```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

using sw model nucleic search, OM nucleic

May 29, 2000, 11:22:12 ; Search time 1446.77 Seconds (without alignments) 11:932 Million cell updates/sec Run on:

US-08-935-377-1 69 1 GGCCAAAAATTGAAAAACTA......GCCCGGCCGCCAACGGCGGA 69 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 seqs, 125096042 residues Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Genesed_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Vaccinia virus 7.5	Vaccinia virus vec	Vaccinia virus pro	Vaccinia virus vec	Ø	Poxvirus ATI promo	н	DNA encoding L-pro	н	Mycoplasma gallise	Mlui-BamHi fragmen		Vaccinia virus ear	e of earl	မိ	early/la		vector 5	B of Sf1	B of Sf1	ector 5	A of Sf1	A of Sfi	vector 5	vector 5		Ing	-	encoding	I fragment	Sfil fragment cont	I fragment e	Promoter for infec
SUMMAKIES		a	532	619	532	619	024	445	445	362	362	469	477	623	893	056	850	964	962	963	894	055	850	894	055	850	962	667	667	667	362	894	057	T48510	328
		8 :	٦	1	~1	1	-	ч	-	Н	Н	, -1		Н	Н	Н	-	Н	Н	Н	Н	Н	Н	Н	Н	1	H	-	-	٦	 1	-	Н		-
	,	Length	9	36	98	98	0	38	38	87	œ	94	40	40	40	40	40	70	0	0	^	^	^	æ	œ	æ	0	S	m	n	æ	17	^	4177	~
		Match	4.	1.4	4	1.4			٠	.7	•			•	•	•		•	•	•	•						•	•	•	•	•	•	•	6.2	
df	Query	Mat	4	4	43	4.		ĕ																										ĕ	
		Score	ω.	φ.	œ.	28.6	۲.	ů.	ė	26	~	ω.	25.4	'n.	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25		24.8
	Result	8	1	7	ю	7	Ŋ	φ	0	œ	σ	10	11	12	13	14	12	16	17	18	19	50	21	22	23	24	25	56	27	28	58	30	31	32	33

ö

M. tuberculosis se Adenovirus E4 and Complete sequence Complete sequence Recombinant adenov Adenoviral vector Recombinant adenov Adenovirus vector Recombinant cis-ac Adenovirus 5 genom Recombinant trans- Human tumour necro
X38293 T31315 T31315 T31315 T60559 T60559 X07371 T60557 T60557 T60557 V07258 V00493
ананананана
1433 3189 8710 10610 32026 34303 34303 34427 35935 36538
~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
22222222222222222222222222222222222222
######################################

## ALIGNMENTS

RESULT 1  065321 standard; DNA; 2360 BP.  AC 065321,  DT 21-DEC-1994 (first entry)  DE 21-DEC-1994 (first entry)  DE 21-DEC-1994 (first entry)  DE 21-DEC-1994 (first entry)  DE 21-DEC-1994 (first entry)  MA milsense; therapy; inhibition; viral protein precursor;  KW HCV core protein; luciferase; fusion construct; ds.  NAC-1933; 10-1046.  DE 25-MG-1992; JP-248796.  PR 23-MG-1993; JP-248796.  PR 03-MAR-1993; JP-042736.  PR 03-MAR-1993; JP-048796.  PR 03-MAR-1993; JP-042736.  PR 03-MAR-1993; JP-048796.  PR 03-MAR-1993; JP-048796.  CALIOLISE SAIL M.  PI HOND Y SEMI W.  PI HOND Y SEMI Y SEMI W.  PI HOND Y SEMI Y SEM	Query Match 41.4%; Score 28.6; DB 1; Length 2360; Best Local Similarity 88.6%; Pred. No. 0.25; Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps Qy 3 CCAAAAATTGAAAACTAGATCTATTATTGCACG 37	RESULT 2 Q86798 ID Q86798 standard; DNA; 2360 BP. AC Q86799 DD Q86799 standard; DNA; 2360 BP. AC Q86799 DD Vaccinia virus vector pHASE. KW vaccinia virus vector; pHASE; hepatitis C virus; T7NI-19; KW antiviral agent; pollovirus; human rhinovirus; KW internal ribozyme entry site; non-A non-B; KW cerebral cardio-hepatitis; foot and mouth disease; ds. OS Vaccinia virus. PN J0706899-A.
--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

```
Q86799 standard; DNA; 4987
                                                                         04-DEC-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                     4987 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; R34635 #
                                                                                                                                                                                                                                 P-PSDB; R72801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoassay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
J05078395-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-AUG-1993
                                                                                                                                                                        J07069899-A
                                                                                                                                                                                                                                                                                                                                                            infections.
                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
Q40242
                                   RESULT
Q86799
ID Q8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                  ò
                                                                                                                                                                                                                        ö
Vaccinia virus promoter and HCV core protein-luciferase fusion gene. Hepatitis C Virus; HCV; control; Non-A, non-B hepatitis virus; antisense; therapy; inhibition; viral protein precursor; recombinant vaccinia virus; HCV core protein gene; firefly; luciferase reporter gene; fusion construct; ds. Chimeric Vaccinia virus. Chimeric Patitis C virus. Chimeric Hepatitis C virus. Chimeric Photinus Pyralis. Exercise Photinus Pyralis.
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti:sense oligo:nucleotide(s) complementary to the hepatitis C virus genome - are useful as antiviral agents
Example 5; Page 243-251; 262pp; English.
A recombinant vaccinta virus which codes for a HCV core protein fused to the firefly luciferase enzyme was constructed from PCR amplified fragments. The construct was useful for assaying the inhibitory activity of various antisense oligonucleotides on HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1332 T;
                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.4%; Score 28.6; DB 1; Length 4987;
88.6%; Pred. No. 0.31;
tive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                      Score 28.6; DB 1; Length 2360;
Pred. No. 0.25;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "encodes HCV core protein-luciferase
fusion protein"
                                                                                                                                                                           693 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1083 G;
                                                                                                                                                                            ö
                                                                                                                                                                            399
                                                                                                                                                                                                                                                          1235 CCAAAAATTGAAAAACTAGTCTAATTTATTGCACG 1269
                                                                                                                                                                                                                                             3 CCAAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1052 C;
                                                                                                                                                                            410 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1520 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA2104649-A.
26-FEB-1994.
23-AUG-1993; 104649.
25-AUG-1993; JP-248796.
03-MAR-1993; JP-042736.
(SEKI/) SEKI M.
HONGA Y, SEKI M, Yamada E;
WPI; 94-151836/19.
                                                                                                                                                                             858 A;
                                                                                                                                                                                                         41.4%;
88.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1826. .4057
/*tag= a
                                                                                                                                                                                                                                                                                                             Q65322 standard; DNA; 4987
Q65322;
                                                                                                                                                                                                                                                                                                                                     21-DEC-1994 (first entry)
                                                                                                                                                                                                                  Best Local Similarity 88.6
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 31; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4987 BP;
                                                                                                                                                                              2360 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene translation.
                                                                                                                                                                     infections.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                RESULT
Q65322
                                                                                                                                                                                                                                                                                                                             ð
```

```
Disclosure, Page 9; 11pp; Japanese.
This sequence is the vaccinia virus early promoter, used when cloning a glycoprotein originating from blood disseminating nonA-nonB
                                                internal ribozyme entry site; non-A non-B; cerebral cardio-hepatitis; foot and mouth disease; ds.
Vaccinia virus vector comprising HCV T7NI-19 and firefly luciferase. Vaccina virus vector; firefly luciferase; hepatitis C virus; T7NI-19; antiviral agent; poliovirus; human rhinovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccinia virus early promoter.
HCV; hepatitis C virus; nonB-nonB hepatitis; NANBHV; vaccinia virus;
VV; cowpox; liver disease; infection; diagnosis; testing; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                 Cultus, polio: virus and human rhinovirus
Disclosure; Pages 19-22; 23pp; Japanese.
086788 encodes R72800 Hepatitis C virus (HCV) T7N1-19, which
disrupts viral gene translation, by preventing the binding of
the viral mRNA to the internal ribozyme entry site. It was
used in the construction of an antiviral agent detecting vector
(Q86799 which encodes R72801, which comprises a vaccinia virus
vector, a vector containing T7N1-19 and a firefly luciferase gene.
The antiviral agent can be used to treat HCV, poliovirus, cerebral
cardio-hepatitis, human rhinovirus and foot and mouth disease viral
                                                                                                                                                                                                                                                                                                                                                                      Antiviral agent comprising component which disrupts viral gene translation - used for the selective inhibition of e.g. Hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1322 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glyco-protein derived from blood disseminating non A non B hepatitis virus - used as diagnostic agent for vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1081 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; DB
0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1235 CCAAAATTGAAAACTAGTCTAATTTATTGCACG 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CCAAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.4%; Score 28.6;
88.6%; Pred. No. 0.
                                                                                                                                            Location/Qualifiers
1826. .4057
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1516 A;
                                                                                                                                                                                                                                          14-MAR-1995.
02-SEP-1993; 241973.
02-SEP-1993; JP-241973.
(MIU ) MITSUBISH! KASEI CORP.
WPI; 95-144713/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             040242 standard; DNA; 207 BP.
040242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.6
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAR-1993,
20-SEP-1991; 241275,
20-SEP-1991; JP-241275.
(JAPG ) NIPPON ZEON KK.
```

Conservative

ö

Gaps

; 0

```
31-MAY-1997 (first entry)

DNA encoding L-proline-3-hydroxylase.

L-proline-3-hydroxylase, L-proline, cis-3-hydroxy-L-proline,
2-ketoglutaric acid; ferrous ion; intermediate; drug; food additive; ds.

Streptomyces sp. strain TH1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence, derived from pTH30, isolated from Streptomyces sp., encodes an L-proline-3-hydroxylase (W09782) which converts L-proline to cis-3-hydroxy-L-proline in the presence of 2-ketoglutaric acid and ferrous ions. The DNA is used for efficient production of cis-3-hydroxy-L-proline on an industrial scale for use as an intermediate in the manufacture of drugs and as a food additive. Sequence 870 BP; 173 A; 299 C; 262 G; 136 T;
                                                                                                                                                      WPI; 94-312814/39.
A poxvirus promoter contg. an ATI promoter and prophase - useful for the production of exotic genes in large quantities for the production of exotic genes in large quantities of 21 10pp. Japanese.
Graffs and 074459 together form a double-stranded nucleotide fragment with overhanging sticky ends. The fragment comprises the ATI promoter and pro-phase expression promoter. Coding sequences (e.g. heterologous coding sequences or homologous sequences such a the poxvirus haemagglutinin gene) can be placed downstream of the promoter fragment for recombinant production of the polypeptides. 38 BP; 12 A; 7 C; 4 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA coding for L-proline-3-hydroxylase of microbial origin - large scale production of 3-hydroxy-L-proline useful as drug intermediate or food additive
/label- sticky_end
/note- "see Q74458 for complementary strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.7%; Score 26; DB 1; Length 870; 70.0%; Pred. No. 1.6; tive 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 CIAGAICTATITATIGCACGCGGCCGCCAIGGGCCCGGCCGCCAACGGCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 26.6; DB
Pred. No. 0.41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AAAAATTGAAAAACTAGATCTATTTATTGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; Page 48; 81pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-1996.
07-MAR-1996.
07-MAR-1995; JP-046987.
(KYOW ) KYOWA HAKKO KOGYO KK.
MOTJ H. OZBAŁ A. Shibasaki T.
P-PSDB; W09782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T63623 standard: DNA; 870 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        38.6%;
87.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T63622 standard; DNA; 1081
T63622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 87.9 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 70.0
Matches 35; .. Conservative
                                                                                                    JP-342362.
                                                            30-AUG-1994.
21-7AN-1993; 008424.
22-DEC-1992; JP-34236
(SHID/) SHIDA H.
(TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
T63622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u></u> 유
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                          ö
               anti-vaccinia virus. NaNBHV originated core and envelope genes were cloned. The resultant 4.01kb plasmid was named pIK4CE and its sequence determined. A recombinant vector contg. vaccinia virus (VV) TK gene with the VV 7.5kb promoter was prepd. This vector contd. VV originating TK gene with the synthetic VV early promoter. A second recombinant vector for the prepn. of VV. having the structural protein gene region of NANBHV was prepd, and used to produce a recombinant VV. The NANBHV protein was expressed in a VV infected cell.
hepatitis virus (NANBHV) and causing an antigen-antibody reaction with
                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A poxvirus promoter contg. an ATI promoter and prophase - useful for the production of exotic genes in large quantities claim 2: Page 2: 10pp; Japanese.
Claim 2: Page 2: 10pp; Japanese.
074458 and 074459 together form a double-stranded nucleotide fragment with overhanding stilcky ends. The fragment comprises the ATI promoter and pro-phase expression promoter. Coding sequences the poxvirus haemagglutinin gene) can be placed downstream of the promoter fragment for recombinant production of the promoter fragment for recombinant production of the posyment sequence 38 BP; 15 AF, 4 C; 7 G; 12 T; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-WAY-1995 (first entry)
Poxvirus AII promoter, nucleotides -32 to +6 (complementary strand).
AII promoter; poxvirus; pro-phase expression; ss.
                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag- a
/label- sticky_end
/note- "see Q74459 for complementary strand"
                                                                                                                                                                                                                                                 Length 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.6%; Score 26.6; DB 1; Length 38; 87.9%; Pred. No. 0.41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                           AAAAATIGAAAAACTATICTAATITATIGCAATAGICGACCATGGCC 125
                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                    AAAAATTGAAAAACTAGATCTATTTATTGCACGCGCCGCCATGGGC
                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATI promoter; poxvírus; pro-phase expression; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poxvirus AII promoter, nucleotides -28 to +10.
                                                                                                                                                                                                                                                 Score 27.8; DB Pred. No. 0.25;
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.43
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                 40.3%;
74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q74459 standard; DNA; 38 BP. Q74459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35. .38
/*tag= a
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q74458 standard; DNA; 38
Q74458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-1994.
21-JAN-1993; 008424.
22-DEC-1992; JP-342362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SHID/) SHIDA H. (TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 94-312814/39
                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J06237773-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
```

ö

Gaps

ö

for

Query Match

ò g RESULT 074459/c

ö

Gaps

ö

Indels

ø

RESULT Q74458

79

ò g

888888888888

DDE PET THE PE

```
Example 1; Fig 2; 30pp; English.

The 5'end of this strand overhangs the 3'end of its complementary strand by 4 bases (1.e. 5'-CGGG-3'); the 5' end of the complementary strand by 4 bases (1.e. 5'-CGGG-3'); the 5' end of the complementary strand overhangs the 3'end of this strand, also by 4 bases (1.e. 5'-CGGG-3'); the double-stranded fragment was lighted to other synthetic fragments containing a multiple cloning site (mcs) and a 2 directional poxvirus early transcriptional termination signal.

These were lighted downstream of a FPV promoter, initiation codon and lacZ gene (from pMC1871 and pMA001). The resulting 3.5kb containing the containing a Skb process. Inserted into vector, (Plasmid pM2173R was made by subcloning a Skb ppil series were eliminated from both junction regions and an mcs was all mcs's were eliminated from both junction regions and an mcs was inserted into 2 adjacent EcoRN fites in the cloned FPV fragment with linkers). A fragment conts, the entire coding region of Marek Disease Virus glycoprotein B homologue (gBh) was inserted into chickens. See also 034774-03478181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Combined pox:virus promoters contain at least four promoter fragments - and pox:virus containing the combined promoters and
                                                                                                                                                                                                                                                                                       24-JUN-1992; 305775.
28-JUN-1992; US-722860.
28-JUN-1991; US-722860.
(JAPG ) NIPPON ZEON KK.
(USDA ) US SEC OF AGRIC.
Liee LF, LI Y, Nazerian K, Ogawa R, Yanagida N;
WPI: 93-001546/OU pox virus contg. Marek's disease virus antigen gene - used to produce cell-free vaccine against Marek's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-1996 (first entry)
Recombinant pox virus E promoter fragment.
promoter; pox virus; combined promoter; recombinant; vaccine; poultry; live; ds.
                                                                                                                           07-MAY-1993 (first entry)
Miul-BamHi fragment of pNZ1729R insertion vector.
Insertion vector; fowlpox virus; FPV; strain NP; MDV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.8%; Score 25.4; D
82.9%; Pred. No. 1.1;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Fig 1; 12pp; Japanese
                                                                                                                                                                                   glycoprotein B homologue; ds Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-1995.
30-AUG-1993; 238953.
30-AUG-1993; JP-238953.
(JAPG) NIPPON ZEON KK.
(SHIO) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q86231 standard; DNA; 40 BP.
                                                                                  Q34776 standard; DNA; 40 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 95-143849/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
J07067655-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   foreign gene
                                                                                                                                                                                                                                                  EP-520753-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                     Day coding for L-proline-3-hydroxylase of microbial origin - for large scale production of 3-hydroxy-L-proline useful as drug large scale production of 3-hydroxy-L-proline useful as drug intermediate or food additive

Claim 3; Page 53-54; Blpp; Japanese.

This Kpil-Ecori fragment, derived from pTH30, which was isolated from Streptomyces sp., contains the open reading frame (T68623) that encodes an L-proline-3-hydroxylase (W09782) which converts L-proline to cis-3-hydroxy-L-proline in the presence of 2-ketoglutaric acid and ferrous ions. The DNA is used for efficient production of cis-3-hydroxy-L-proline on an industrial scale for use as an intermediate in the manufacture of drugs and as a food additive.

184 365 C; 334 G; 164 T;
03-JUN-1997 (first entry)
Kphl-EcocRi fragment of pTH30 encoding L-proline-3-hydroxylase.
L-proline-3-hydroxylase; L-proline; cls-3-hydroxy-L-proline;
2-ketoglutaric acid; ferrous ion; intermediate; drug; food additive; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A new antigenic protein which reacts with Mycoplasma gallisepticum is useful in a component vaccine for use against poultry infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is useful in a component vaccine for use against poultry infected with M. gallisepticum. Example 1; Page 8; 33pp; Japanese. 094699 is a promoter for the Mycoplasma gallisepticum antigenic protein TM-16 gene. TM-16 can be used as a vaccine for M. gallisepticum infectious diseases in poultry, and as a diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-1996 (first entry)
Mycoplasma gallisepticum antigenic protein TM-16 gene promoter.
Antigenic protein; vaccine; poultry; diagnosis; TM-16;
promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491 CGAGATCTGGTTCCTCGACGCGGCCGCCGTCCACTCGGCCGTCAACTTCG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.0%; Pred. No. 1.7;
Matches 35; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 CTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAACGGCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAAATTGAAAAACTATTCTAATTTATTGCACTCGTC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.4%; Score 25.8;
81.1%; Pred. No. 1;
                                                                                       11 C;
                                                                                                                                                                                                                                                     07-WAR-1996; J00558.
07-WAR-1995; JP-046987.
(KYOW) KYOWA HAKKO KOGYO KK.
MOLI H, OZAKI A, Shibasaki T;
WPI; 96-425428/42.
P-PSDB; W09782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q94699 standard; DNA; 94 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agent for M. gallisepticum.
Sequence 94 BP; 32 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SHIO ) SHIONOGI & CO LTD. WPI; 95-220782/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-1993; 213102.
27-AUG-1993; JP-213102.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                         WO9627668-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             094699;
```

RESULT 10

a a

ò

094699

28

엄 ð

ö

Gaps

ö

9

DB 1; Length 40; Indels į.,

```
WPI; 94-294008/36.
New recombinant fowl pox viruses - useful as vaccines against
fowl pox virus, Newcastle Disease Virus and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 29, 2000, 21:58:06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9640880-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                               ö
The DNA shown is a pref. DNA fragment with E (early) promoter activity, which is used in the construction of a combined promoter for recombinant poxvirus. Combined promoters for poxvirus comprise at least four DNA fragments having a promoter activity, pref. these fragments have early and late activity, and the promoter has at least one, pref. more than two promoters. The combined promoter has a strong activity and hence is useful in an effective vaccine, esp. against poxvirus in poultry. Sequence 40 BP: 15 A; 7 C; 5 G; 13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant fowl pox virus for use in vaccines - contains genes expressing antigens of Newcastle disease virus and opt.

Thectious bronchitis virus
Infectious bronchitis virus
Disclosure, Page 62; 85pp; English.

Synthetic pox viral promoters were constructed for recombinant fowlpox vectors. The four promoter cassettes - EPI, LPI, EP2 and LP2.

Care based on promoters that have been defined in the Vaccinia virus.

C Each cassette was designed to contain DNA sequences defined in Vaccinia flanked by restriction sites. Initiator Mets were also designed into each cassette such that in frame fusions could be made at either EcoRI or BamHI sites. A set of translational stop codons in all three reading frames and an early transcriptional termination signal was also engineered downstream of the in-frame fusion site.

Sequence 40 BP; 17 A; 5 C; 5 G; 13 T;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-1995 (first entry)
Sequence of early promoter cassette EP1.
Early promoter; synthetic pox viral promoter; fowlpox; vaccinia; ss.
                                                                                                                                                                               ö
                                                                                                                                                  Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36.2%; Score 25; DB 1; Length 40; 84.8%; Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                         13-APR-1995 (first entry)
Vaccinia virus early promoter cassette EP1.
Early promoter; cassetter; recombinant fowlpox vector; synthetic pox promoter; ss.
                                                                                                                                                                             9;
                                                                                                                                                  DB 1;
                                                                                                                                                                                                                           6 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 40
                                                                                                                                                                                                           5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                Score 25.4; D
Pred. No. 1.1;
                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AAAAATIGAAAAACTATICTAAITTAIIGCACG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                               Query Match 36.8%;
Best Local Similarity 82.9%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q70568 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                              Q68938 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  01-SEP-1994.
28-FEB-1994; U01826.
26-FEB-1993; US-024156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JAPC ) NIPPON ZEON KK.
(SYTR ) SYNTRO CORP.
Cochran MD;
WPI; 94-294007/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-SEP-1994.
28-FEB-1994; U02252.
26-FEB-1993; US-024156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
WO9419015-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      070568;
                                                                                                                                                                                                                                                                                 RESULT
Q68938
   888888888
                                                                                                                                                                                                            à
                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DA CARE DA CAR
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
T frowl pox virus, vercus-

T laryngotrachefits virus.

I laryngotrachefits virus.

S bisclosure, Page 71; 97pp; English.

Disclosure, Page 71; 97pp; English.

C Four promoter cassettes were designed based on promoters that have been defined in vaccinia virus. These are EPI, LPI, EP2 and LP2.

C Goods, 070571, 070572 and 070569 respectively. Each cassette was consident to contain the DNA sequences defined in vaccinia flanked by crestriction sites which could be used to combine the cassettes in any order or combination. Initiator Mets were also designed into compose to cassette such that inframe fusions could be made at either cassette such that inframe fusions could be made at either construction and an early translational stop codons in all three reading frames and an early transcriptional termination signal composer and an early transcriptional termination signal construction of the inframe fusion site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccines.
Disclosure; Page 101; 134pp; English.

4 Promoter cassettes (148506-09) are based on promoters that have been defined in vaccinia virus. They respectively comprise early promoter 1 (EPI), early promoter 2 (EP2) and late promoter 2 (LP2).

Form of late promoter 2 (LP2). The promoters offer several advantages including the ability to control the strength and timing of foreign gene expression, and have been utilised in recombinant fowlows virus vectors (see also T48502-03) to control expression of foreign DNA. Recombinant fowlow viruses can be used as vectors for the delivery of specific vaccine antigens or cytokines to animals, esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic early promoter 1 (EP1). Fowlpox virus; FPV; recombinant virus; vector; vaccine; poultry; immunisation; Newcastle disease virus; NDV; promoter; EP1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cochran MD, Junker DE, Singer PA;
WPI: 97-087060/08.
New recombinant fowlpox virus - contg. a foreign DNA sequence
inserted into the fowlpox virus genome, used for the prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.2%; Score 25; DB 1; Length 40; 84.8%; Pred. No. 1.6; 1.0e 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 1; Length 40;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAAATTGAAAACTAGATCTATTTTTTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.2%;
Best Local Similarity 84.8%;
Matches 28; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T48506 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.2
Best Local Similarity 84.8
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-DEC-1996.
04-JUN-1996; U11187.
07-JUN-1995; US-484790.
(SYTR ) SYNTRO CORP.
```

Job time: 38154 sec

us-08-935-377-1.rng

Н

```
Sequence 6, Appli
Sequence 16, Appli
Sequence 3, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 28, Appli
Sequence 15, Appli
Sequence 15, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 10, Appli
Sequence 32, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
Sequence 33, Appli
                                                                                May 29, 2000, 11:23:19 ; Search time 621.83 Seconds (without alignments) 14.424 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                       US-08-935-377-1
69
1 GGCCAAAATTGAAAAACTA......GCCCGGCCGCCAACGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_NA:*

.. /cgnl_6/ptodata/1/ina/5A_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/5B_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/5C_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/5C_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/5C_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/pcTuS_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/PcTuS_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/PcTuS_COMB.seq:*
.. /cgnl_6/ptodata/1/ina/Packfilesl.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-803-633A-6

US-08-52-742-16

US-08-525-742-30

US-09-287-375-3

US-09-287-375-3

US-09-287-375-13

US-08-525-742-28

US-08-525-742-29

US-08-525-742-15

US-08-525-742-15

US-08-525-742-15

US-08-525-742-15

US-08-525-742-15

US-08-525-742-15

US-08-525-742-15

US-08-525-742-15

US-08-640-640-10

US-08-484-525-8

US-08-640-640-10

US-08-640-640-10

US-08-640-640-10

US-08-640-10

US-08-640-640-32

US-08-640-640-32

US-08-680-554A-32

US-08-680-554A-32

US-08-680-554A-32

US-08-680-554A-32

US-08-640-640A-32

US-08-640-640A-32

US-08-640-640A-32
                                                                                                                                                                                                                                                                   hits satisfying chosen parameters:
                                                                                                                                                                                                                                          230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        nucleic search, using sw model
                                                                                                                                                                                                  IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ᲐᲡᲡപᲡᲡ4ᲡᲐᲑᲡᲡപെ
                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
25
25
25
25
25
25
25
25
25
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                      Database : .
                                                        OM nucleic
                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                           Searched:
                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O
```

sequence 78, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 21, Appl		
US-08-097-554A-78 US-08-480-640A-78 US-08-484-575A-16 US-08-477-459-16 PCT-US94-01826A-16 PCT-US94-01826A-16 US-08-097-554A-04 US-08-407-459-15 US-08-407-459-15 US-08-407-459-15 US-08-407-459-15 US-08-407-459-15 US-08-407-459-15 US-08-400-640A-15 US-08-097-554A-12 US-08-480-640A-15 US-08-480-640A-15 US-08-480-640A-15 US-08-480-640A-11 US-08-480-640A-11 US-08-480-640A-11 US-08-480-640A-11 US-08-480-640A-11 US-08-480-640A-11		. VACCINE FOR MAREK'S DISEASE BIRCH Street
459441 459441 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995 45995	NTS	, 2 m m
784 784 784 785 785 785 785 785 785 785 785	NWE	Soru Soru AGAINST J HASCH & J Hington (), 633A
8 8 8 8 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALIGNMENT	3633A 69025oru NANT FOWLPOX ION AGAINST O' KOLASCH & MS-DOS e #1.0, Vers /803,633A M. 77 1644-103P
US-1		US/078036338 Keyvan F. No5369022 Ohel', Ohel', SECOMBINANT PROTECTION R 19 S: STEWART, KOI 69025th Wash Ompatible PC-DS/MS-DC STEWART, KOI 69025th Wash ATS. US/07/803, 210 ATION: Gerald M. ATION: Gerald M. 44.1300 -28,977 WHER: ORMATION: Gerald M. 44.1300 -2848 10CS: irs
w N 4 N 0 0 W 4 N N 0 0 N H W N 0 4 N		S/0780: Keyvan F: 53( Tel 1, 53( Tel 1, 53( Tel 1, 53( Tel 1, 53( Tel 2, 53( Tel 2, 63( Tel 3, 63( Tel 3
111 111 178 178 178 182 182 182 182 182 206 206 206 4177		-633A-6/C -633A-6/C -634D1cation US/07803633A No. 5360025 LINEORMATION: LICANT: NAZERRAN, Keyvan LICANT: LEE, Lucy F. LICANT: DEG, Lucy F. LICANT: OGAWA, Ryohei, EER OF SEQUENCES: 19 EER OF SEQUENCES: 19 EER OF SEQUENCES: 19 EER OF SEQUENCES: 10 UNTRY: Falls Church ATE: VITGINIA UNTRY: LAIS CHURCH ATE: VITGINIA UNTRY: LEADABLE FORM: UNTRY: LAIS COMPATIBLE EERT APPLICATION DATA: LING DATE: 19911210 ASSIFICATION NUMBER: 1644-10 GIGTRATION NUMBER: 18,977 LING DATE: 19911210 ASSIFICATION INFORMATION: ME: MULPHY JT., Gerald M. GIGTRATION INFORMATION: LEFRA: 246345 ATION FOR SEQ ID NO: 6: EERCE CHARCTERISTICS: NUCLEIC ACID EER NUCLEIC ACID EER NUCLEIC ACID EER NUCLEIC ACID ESTANDENCES: single
aaaaaaaaaaaaaaaaaaaa		/c MAJICATION: NAZERIA: NAZERIA: NAZERIA: LIEW, LOSA CGAWA, LI, YI VENTION: CBUTCES SENTE NO. 1151 CHUT 1151 CHUT 11
00000000000000000000000000000000000000		1-6/c 369025 369025 3789025 3789025 3789025 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 3789026 37
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		SULT 1  10.07-803-633A-6/C  Sequence 6, Application US/07803633A  Patent No. 5369025  GENERAL INFORMATION:  APPLICANT: LEE, LUCY F.  APPLICANT: LEE, LUCY F.  APPLICANT: GAWA, RYOHE!  APPLICANT: LIL YI  TITLE OF INVENTION: PROTECTION AGAINS  NUMBER OF SEQUENCES: 19  CORRESPONDENCE DDDESS:  ADDRESSE: BIRCH, STEWART, KOLASCH STREFT: 301 NO. 5369025th WashingtC  CITY: Falls Church STREFT: 301 NO. 5369025th WashingtC  CITY: Falls Church STATE: VIFGINA  LIP 22040-0747  COMPUTER: LEM PC Compatible  OPERATING SYSTEM: PC-DOS/MS-DOS  SOFTWARE: Patentin Release #1.0, Ve  CURRENT APPLICATION NUMBER: US/07/803,633A  APPLICATION NUMBER: US/07/803,633A  APPLICATION NUMBER: 1844-103P  TELECOMMUNICATION: RECORDERTION:  REGISTRATION: RECORDERTION:  REGISTRATION: RECORDERTION:  REGISTRATION: RECORDERTION:  TELERAX: (703) 241-2848  TELECOMMUNICATION INFORMATION:  TELECOMUNICATION INFORMATION:  TELECOMUNICAT
777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 - 777 -		RESULT 1 Sequence   Patent No

ö

Gaps

ö

Length . Indels

40,

ä

Query Match 38.3%; Score 26.4; DB Best Local Similarity 83.3%; Pred. No. 0.39; Matches 30; Conservative 0; Mismatches

ò

```
APPLICANT: Saito, Shuji
APPLICANT: Saeti, Satiko
APPLICANT: Ohkawa, Setsuko
APPLICANT: Saeki, Sakiko
APPLICANT: Saeki, Sakiko
APPLICANT: Saeki, Sakiko
APPLICANT: Iritani, Yoshikazu
APPLICANT: Iritani, Yoshikazu
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: PULYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
WINDER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND & ADDRESSEE: NAUGHTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING PATENT PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 26.4; DB 3;
Pred. No. 0.49;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 AAAAATTGAAAAACTATTCTAATTTATTGCACTCGG 4
CURRENT APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSPIRCATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-194
ATTORNEY/AGENT INFORMATION:
NAME: MCLELAND, LE-NNUMB
REGISTRATION NUMBER: 31,541
REPERNICE/DOCKET NUMBER: 950811
FELECOMMUNICATION INFORMATION:
TELEPHONE: 020-59-9330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   other nucleic acid
/desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1725 K Street, Suite 1000
                                                                                                                                                                                              Sequence 30, Application US/08525742 Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-8870357
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tinear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-525-742-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                        33
                                           요
                                                                                                                                                                                                                                                                                                                                          APPLICANT: Salto, Shuji
APPLICANT: Salto, Stelko
APPLICANT: Saeki, Sakiko
APPLICANT: Obsawa, Ikuroh
APPLICANT: Obsawa, Ikuroh
APPLICANT: Tittani, Yoshikazu
APPLICANT: Aoyama, Shigemi
APPLICANT: OF INVENTION: RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND & ADDRESSEE: NAGSTRONG STREET: 1725 K Street, Suite 1000 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BIR PC compatible
COMPUTER: BIR PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

38.3%; Score 26.4; DB 3;

Best Local Similarity 83.3%; Pred. No. 0.39;

Matches 30; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGG 40
                                                        5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGG
                                                                                                                    39 AAAAATTGAAAAACTATTCTAATTTATTGCACTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00541
FILING DATE: 31-MAR-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOTUMARE: Patentin Release #1.0, NCURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                           Sequence 16, Application US/08525742
Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: McLeland, Le-Nhung
REGISTRATION NUMBER: 31,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-659-2930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202-8870357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: TELEFAX: 2
                                                                                                                                                                                                                                                       -08-525-742-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-525-742-16
                                                                                                                        셤
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 CTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAACGGCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/287,375 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
GENERAL INFORMATION:
APPLICANT: OZAKI, AKIO
APPLICANT: MOII, Hideo
APPLICANT: MOII, Hideo
APPLICANT: Moil, Hideo
APPLICANT: OCHAI, Ketko
APPLICANT: OCHAI, TERRY CANTEN
STREEPONDENCE: ANTONELLI, TERRY CANTENT
STREEPONDENCE: ANTONELLI, TERRY CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : ANTONELLI, TERRY, STOUT AND KRAUS
1300 NORTH SEVENTEENTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.7%; Score 26; DB 5 Best Local Similarity 70.0%; Pred. No. 1.2; Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT.?'6
US-08-708-856A-13
; Sequence 13, Application US/08708856A
; Patent No. 5663254
; GENERAL INFORMATION:
; APPLICANT: Ozaki, Akio
; APPLICANT: Mor1, Hideo
; APPLICANT: Shibasaki, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1300 NORTH SEVENTEENTH STE
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces sp. STRAIN: TH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 CGAGATCTGGTTCCTCGACGCGCCGCCGTCCACTCGGCCGTCAACTTCG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 37.7%; Score 26; DB 4; Length 870; Best Local Similarity 70.0%; Pred. No. 1.2; Matches 35; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAACGGCG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1300 NORTH SEVENTEENTH STREET
COUNTRY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22209
COMPUTEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,856A
FILING DATE:
                                                                   Sequence 3, Application US/08708856A
Sequence 3, Application US/08708856A
GENERAL No. 5963254
APPLICANT: CARKI, Akio
APPLICANT: Mori, Hideo
APPLICANT: Ando, Katsuhiko
APPLICANT: Ando, Katsuhiko
APPLICANT: Ochiai, Keiko
APPLICANT: Chiba, Shigeru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/301,654
FILING DATE: 07-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 248545
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 870 base paires
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: genomic DNA ORIGINAL SOURCE: ORGANISM: Streptomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; STRAIN:
US-08-708-856A-3
```

Gaps

US-09-287-375-3 ; Sequence 3, Application US/09287375

```
GENERAL INFORMATION:
APPLICANT: Saich, Shuji
APPLICANT: Saich, Sakiko
APPLICANT: Okawa, Setsuko
APPLICANT: Ohawa, Ikuroh
APPLICANT: Tiftani, Yoshikazu
APPLICANT: Takahashi, Kiyoohito
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: NEW POLYPEPTIDE, DNA ENCODING THE
TITLE OF INVENTION: PROCOMBINANT VECTOR BEARING THE DNA AND
TITLE OF INVENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
VUMBER OF SEQÜENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.7%; Score 26; DB 5; Length 1081; Best Local Similarity 70.0%; Pred. No. 1.3; Matches 35; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAACGGCG 67
                                                                                                                                                                                   ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/287,375
FILING DATE:
                                                            ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS STREET: 1300 NORTH SEVENTEENTH STREET
Cis-3-Hydroxy-L-Proline
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/708,856
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/474,135
FILING DATE: 07-JUN-1995
CLASSIFICATION
ATTORNEY/AGENT INFORMATION:
NAME: TETY DAVIG T.
REGISTRATION NUMBER: 20178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.508-525-742-28/C
; sequence 28, Application US/08525742
; Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPAX: 703-312-6666
TELEFX: 703-312-6666
TELEX: 248545
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORTGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1081 base paires
TYPE: nucleic acid
STRANDEDNESS: double
                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
    INVENTION:
                                                                                                               CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.7%; Score 26; DB 4; Length 1081; 70.0%; Pred. No. 1.3; Live 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 CTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAACGGCG 67
                                                                                APPLICANT: Uosaki, Youichi
TILLE OF INVENTION: Process for Producing
TILLE OF INVENTION: Cis-3-Hydroxy-L-Proline
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANTONELLI, TERRY, STOUT AND KRAUS
STREET: 1300 NORTH SEVENTEENTH STREET
CITY: ARRINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                      ZIP: 22209
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/708,856A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICAWT: OZAKI, Akio
APPLICANT: Mori, Hideo
APPLICANT: Shibasaki, Takeshi
APPLICANT: Ando, Katsuhiko
APPLICANT: Ochiai, Keiko
APPLICANT: Ochiai, Shigeru
APPLICANT: Usaki, Youlchi
TITLE OF INVENTION: Process for Producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PELLING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NOTE:
CLASSIFICATION NOTE:
PILING DATE: 07-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION A35
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER: 08/474,135
PRIOR APPLICATION:
NAME: TELY, David T.
REGISTRATION NUMBER: 20178
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1703-312-6660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13, Application US/09287375; Patent No. 6010891; GENERAL INFORMATION: APPLICANT: MOZAKI, Akio APPLICANT: MOZI, Hideo APPLICANT: Shibasaki, Takeshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1081 base paires
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
ORIGINAL SOURCE:
ORGANISM: Streptomyces sp.
            Ando, Katsuhiko
Ochiai, Keiko
Chiba, Shigeru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.09
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-708-856A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-287-375-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

ô

```
Sequence 5, Application US/07803633A

Sequence 5, Application US/07803633A

Patent No. 3569025

GENERAL INFORMATION:
APPLICANT: NAZERIAN, Keyvan
APPLICANT: LEE, Lucy F.
APPLICANT: OGAWA, Ryohei
APPLICANT: LI, YY
TITLE OF INVENTION: RECOMBINANT FOWLPOX VACCINE FOR
TITLE OF INVENTION: PROTECTION AGAINST MAREK'S DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSED:
ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                        STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN BC-BOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 32-SEP-1995
CLASSIFICATION NUMBER: US/08/525,742
PRIOR APPLICATION NUMBER: 19 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: 19 05-245625
FILING DATE: 31-MAR-1993
PRIOR APPLICATION NUMBER: 31.541
APPLICATION NUMBER: 31.541
REFERENCE/DOCKET NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 31,541
RELEPRAK: 202-659-2330
TELEPRAK: 202-689-2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.4%; Score 25.8; D
Best Local Similarity 81.1%; Pred. No. 0.8;
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AAAAATTGAAAAACTATTCTAATTTATTGCACTCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic DNA"
US-08-525-742-27
1: NAUGHTON
1725 K Street, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SECTION 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                             Washington
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
US-07-803-633A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saeki, Sakiko
Ohsawa, Ikuroh
Iritani, Yoshikazu
Aoyama, Shigemi
Takahashi, Kiyoohito
VENTION: ROLYPEPTIDE, DNA ENCODING THE
VENTION: POLYPEPTIDE, RECOMBINANT VECTOR BEARING THE DNA AND
VENTION: RECOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
VENTION: RSCOMBINANT VIRUS UTILIZING THE RECOMBINANT VECTOR AS WELL
EQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND &
                             ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND ADDRESSEE: NAUGHTON STREET: 1725 K Street, Suite 1000 CITY: Washington
                                                                                                                                                                                                                                                                     ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 25.8; DB 3;
Pred. No. 0.79;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIORA APPLICATION 1974
PRIOR APPLICATION 1974
PRIOR APPLICATION NUMBER: JP 05-074139
PRIOR APPLICATION NUMBER: JP 05-245625
PRIOR APPLICATION NUMBER: JP 05-245625
PRIOR APPLICATION NUMBER: JP 05-245625
PRIOR APPLICATION NUMBER: PCT/JP94/00541
FILING BATE: 31-MAR: 1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLELAND, LE-Nhung
REGISTRATION NUMBER: 31.541
REFERENCE/DOCKET NUMBER: 950811
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NESOLY
Sequence 27, Application US/08525742
Sequence 27, Application US/08525742
Sequence 27, Application US/08525742
Setent No. 5871742
GENERAL INFORMATION:
APPLICANT: Saito, Shuji
APPLICANT: Obkawa, Setsuko
APPLICANT: Saeki, Sakiko
APPLICANT: Funato, Hirono
APPLICANT: Funato, Hirono
APPLICANT: Initani, Yoshikazu
APPLICANT: Takahashi, Kiyoohito
TITLE OF INVENTION: POLYPEPTIDE
TITLE OF INVENTION: RECOMBINANT VIR
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 37.4%;
Best Local Similarity 81.1%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 93 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-525-742-28
                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
```

Gaps

```
APPLICANT: Sally, Shirly
APPLICANT: Sally
APPLICANT: Sakin, Sakino
APPLICANT: Ohsawa, Ikuroh
APPLICANT: Ohsawa, Ikuroh
APPLICANT: Tritani, Yoshikazu
APPLICANT: Tritani, Yoshikazu
APPLICANT: Tritani, Yoshikazu
APPLICANT: Tritani, Yoshikazu
APPLICANT: Tritani, Mew Pollyeptide, DNA ENCODING THE
TILLE OF INVENTION: NEW POLLYEPTIDE, DNA ENCODING THE
TILLE OF INVENTION: RECOMBINANT VIRUS OTILIZING THE RECOMBINANT VECTOR AS WELL
TITLE OF INVENTION: AS USE THEREOF
TITLE OF INVENTION: AS USE THEREOF
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND &
ADDRESSEE: NAUGHTON
STREET: 1725 K Street, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20006
COMPUTER REABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.8%; Score 25.4; DB
82.9%; Pred. No. 0.88;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AAAATIGAAAACIATICIAATITATIGCACICG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAPELICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "synthetic DNA"

US-08-525-742-15
                                                             PCT/JP94/00541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 29, Application US/08525742
; Patent No. 5871742
                                                                                                                                                          NAME: MCLELAND, LE-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/OCKET NUMBER: 9508;
TELEPROCOMMUNICATION INFORMATION:
TELEPRA: 202-659-2930
TELEPRA: 202-6890357
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                      FILING DATE: 31-MAR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%
Best Local Similarity 82.9%
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
FILING DATE: 30-SEP-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Salto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 12
US-08-525-742-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Saito, Shuji

APPLICANT: Saito, Shuji

APPLICANT: Saeki, Sakiko

APPLICANT: Ohsawa, Ikuroh

APPLICANT: Punato, Hirono

APPLICANT: Punato, Hirono

APPLICANT: Iritani, Yoshikazu

APPLICANT: Takanshi, Kiyoohito

TITLE OF INVENTION: POLYPEPTIDE, DNA ENCODING THE

TITLE OF INVENTION: POLYPEPTIDE, DNA ENCOMBINANT VECTOR AS WELL

TITLE OF INVENTION: AS USE THEREOF

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADBRESS:

CORRESPONDENCE ADBRESSE ADBRESS:

CORRESPONDENCE ADBRESSE ADBRESSE ADBRESSE ADBRESS:

CORRESPONDENCE ADBRESSE AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: ARMSTRONG, WESTERMAN, HATTORI, MCLELAND ADDRESSEE: NAUGHTON
       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/803,633A
FILING DATE: 19911210
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MULPHY JT., Gerald M.
REGISTRATION NUMBER: 28,977
REBERBNCE/DOCKET NUMBER: 28,977
REDEROCOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.4; DB Pred. No. 0.88; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPLICATION NUMBER: US/08/525,742
FILING DATE: 25-SEP-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-074139
FILING DATE: 31-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 05-245625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: NAUGHTON
STREET: 1725 K Street, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15, Application US/08525742 Patent No. 5871742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 36.8%;
Best Local Similarity 82.9%;
Matches 29; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: NUCLEIC BASE
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
US-07-803-633A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY:
STATE:
```

ò g

```
Sequence 8, Application PC/TUS9401826A
GENERAL INFORMATION:
APPLICANT: Syntro Corporation, et al.
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and Uses Thereof
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSE:
ADDRESSEE: John P. White
STREET: 30 Rockéfeller Plaza
CITY: New York
                                                                                                                                                                                                                                                APPLICANT: Mark D. Cochran
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCE: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10036
COMPUTER READAELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOCOMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,459
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 25; DB 84.8%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                  5 AAAAATIGAAAAACTAGAICTATITATIGCACG 37
                                                                                                                                                                                                                                                                                                                                                               E: John P. White
1185 Avenue of the Americas
                                                                                                                                                          US-08-477-459-8; Application US/08477459; Sequence 8, Application US/08477459; Patent No. 6001369; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 36.2
Best Local Similarity 84.8
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGIH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                    ADDALL
STREET: 1182...
CITY: New York
STATE: New YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ANTI-SENSE: NO
US-08-477-459-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
PCT-US94-01826A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: N. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Mark D. Cochran and David E. Junker
TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
CORRESPONDENCE: 442
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 36.2%; Score 25; DB 4; Length 40; Best Local Similarity 84.8%; Pred. No. 1.2; Matches 28; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CUMTRY: USA

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TPEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,575A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTONREY/AGENT INFORMATION:
NAME: White Esq. John P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)78-0450
TELEFAN: (212)78-0450
TELEFAN: (212)78-0450
SEQUENCE CHARACTERISTICS:
LEGOTH: 40 base pairs
"VPE: nucleic acid
"VPE: nucleic acid
"VPE: "AMIC)
"VPE: "AMIC)
"VPE: "AMIC)
"AMIC)
"AMIC AND TRANCE TRANCE TO TO NO: 8:
SEQUENCE CHARACTERISTICS:
LEGOTH: 40 base pairs
"VPE: nucleic acid
"VPE: "AMIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 36.8%; Score 25.4; DB 3; Best Local Similarity 82.9%; Pred. No. 1.1; Matches 29; Conservative 0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 95
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: John P. White
F: 1185 Avenue of the Americas
New York
         PCT/JP94/00541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08484575A Patent No. 5925358
APPLICATION NUMBER: PCT/UP94/C
FILING DATE: 31-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCLELand, Le-Nhung
REGISTRATION NUMBER: 31,541
REFERENCE/DOCKET NUMBER: 95081
TELECOMMUNICATION INFORMATION:
TELEFAM: 202-659-2930
TELEFAM: 202-659-2930
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 95 base pairs
TYRE: nucleic acid
STRANBEDENES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                    US-08-525-742-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: N
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         윱
```

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAYA:
PPLICATION NUMBER: PCT/US94/01826A
FILING DATE: 28-FBE-1994
CLASSIFICATION:
NAME: White Esq. John P
TELECOMMUTACATION INFORMATION:
NAME: White Esq. John P
TELECOMMUTACATION INFORMATION:
TELECOMMUTACATION INFORMATION:
TELEDAN: (212)664-0525
TELEBAX: (212)64-0525
TELEBAX: (212)64-0525
TELEBAX: (212)64-0525
TELEBAX: (212)64-0525
TELEBAX: (2012)64-0525
TYPE: nucleic acid
```

Search completed: May 29, 2000, 22:08:49 Job time: 38730 sec

1

```
24.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                                                                                                                                                                                                                                                            Re
                                                                              May 29, 2000, 11:21:08; Search time 1214.87 Seconds (without alignments) 432.625 Million cell updates/sec
                                                                                                                                     US-08-935-377-1
69
1 GGCCAAAAATTGAAAAACTA......GCCCGGCCGCCAACGGCGGA 69
                                                                                                                                                                                                                                                                 1765538
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                     882769 segs, 3808571567 residues
                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_ow:*
gb_bov:*
gb_pat:*
gb_pl:*
gb_pl:*
gb_pl:*
gb_pri:*
gb_pri:*
gb_pri:*
gb_pri:*
gb_ro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_sy:*
em_un:*
em_un:*
gp_htg1:*
gb_htg2:*
gb_in1:*
gb_in2:*
em_ba1:*
em_ba2:*
em_ba3:*
                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_pr4:*
gb_htg3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_pat:*
em_ph:*
em_pl:*
em_ro:*
em_rsts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_hum4:*
                                                                                                                                                                                                                                                                                                                                                                                                          gb_ba1:*
gb_ba2:*
                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*
                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                     Searched:
                                                                                  Run on:
```

44: gb_htg6:*
45: gb_htg7:*
46: gb_htg7:*
47: em_htg2:*
48: em_htg3:*
49: em_htg3:*
51: gb_p1:*
52: gb_htg8:*
53: gb_htg9:*
55: gb_htg1:*
55: gb_htg1:*
56: gb_htg1:*
56: gb_htg1:*
56: gb_htg1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

U	n	
ř	÷	
۲	4	
•	3	
2	4	
۲	ζ	
7	5	
2	ď	
L	j	
Ū	'n	
_	1	

	escriptio	1 A part of	3872 DNA enco	04525 Vaccinia v	991 ATI promot	992 ATI	35285 Se	5298 S	827 Homo	189 Strept	5688 Homo	ouenbes 96	595 Sequenc	51 Syntheti	584 Seguence	Poxvirus	397 Sednence	op Eggdrop	98 Avian aden	185 Sednenc	169 Sequenc	1179 Sednenc	209 Sequenc	00 Sednenc	74 Sequence	130 Homo sap	4 Synthetic	Mycobacter	8 Adenoviru	9 adenovir	Sequence 4	8 Caenorhabd	stadeno	/ Adenovirus	645 Homo s	361 Homo	806 Homo s	93 Agrobacte		546 DNA	978 Binary v	19064 Homo sa	AC009731 Homo sap	035318 S	19 Segue	7744 Ral
	Ω	E08871	E08872	E04525	E07991	E07992	AR035285	AR035298	AP000827		AC016688	AR035296	AR035295	E12061	AR035284	EORB48	AR035297	'	VEDS	3418		3417	AR034209	$\circ$	74	Ξ.			AD5004	ADRA	2460	٠.	ADRCOMPGEN		AC023645	236	AC01880	TACH	2	00546	1849	31906	AC00973	03531	3531	ARBCA
	DB	: 5		'n					ď		N			4			,	، م	16	ın ı	ı,	'n	ហ			2	7		o ·	16	S C	34	16	9	2	20	23	-	ഗ	Ŋ		44		'n	Ŋ	7
	gth	23	σ	207	38	38	40	96	œ	53	m	93	97	36	40	040	١	30	$^{\circ}$	70	102	108	111	182	3	152453	∾.	71	ທ	ഗ	5	47	35935	מי	669	6/	171	5	45	5.	92	24	2	86		2080
ф	tc	41.4	41.4	ö	œ.	ش	œ,	œ.	œ.	^	7	۲.	_	٠,	٠.	٠,	٠ ف	٠,		۰	٠.		6	٠.	Ġ	ė	ر. س	٠. ا	ທ. ເຄ		ن	ď.		'n,	'n	ر د	δ.	'n	ŝ	'n	S.	δ.	'n.			
	ore	28.	ω,	27.8	ė.	ė	ů.	è.	è.	56	7	25.8	ď.	'n.	٠. د	٠	ທ່າ		ທີ່				25			7	4	₹.	4	4	4.	4	24.8	4	÷	4	4	4	4	4.	4	4.	4	4	24:4	24.4
	esult No.		8	e	4			0 7		σ	c 10	-	12	13	<b>7</b>	12	10	17	81	61	20	21	55	23	C) I	c 25	56	27	58	53	30	31	3 3	ייני	34	35	m	m	ი 38	m	40	41 .	42	43	44	45

ALIGNMENTS

Location/Qualifiers

```
1826. .4057
                         source
                                                                                                                                                1511 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99
 Key
                                                                FT
FH
FT
FT
                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                           source
                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                          RESULT
E04525
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E08872 4987 bp DNA PAT 29-SEP-1997
DNA encoding a fusion protein of Vaccinia virus protein, HCV protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                      A part of genomic sequence of Vaccinia virus.

A part of genomic sequence of Vaccinia virus.

B08871
B08871.
G1:2176975
JP 1995069899-A/3.
Vaccinia virus.
Vaccinia virus.
Vaccinia virus.
Vaccinia virus.
Vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCE I (bases I to 4987)

O'GS Seki,M., Honda,Y. and Yamada,S. .

E ANTIVIRAL AGENT

MITSUBISHI CHEM CORP

MITSUBISHI CHEM CORP

OC Artificial sequences.

PN JP 199506989-A/4

PD 14-MAR-1995

PF 02-SEP-1993 JP 1993241973

PI SEXI MAKOTO, HONDA YOSHIKAZU, YAMADA SUGURU

PC AGIN31/70.AGIN48/00,CO777/00,C12N15/09//CO7H21/04; CC

c topology: Linear.
                                                                                                                                                                                                                                           os Unknown (Vaccinia virus)
PN 1995069899-4/3
PN 14-MAR-1995
PP 02-SEP-1993 JP 1993241973
PI SEKI MAKOTO, HONDA YOSHIKAZU, YAMADA SUGURU
PC A61K31/70,A61K48/00,C07K7/00,C12N15/09//C07H21/04; CC
topology: Linear;
FH Key
FT Source /organism='Unclassified'
FT Source /organism='Unclassified'
FT FT SOURCE /COMMENTIAM='Unclassified'
FT /Clone='PHASE'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.6; DB 5; Length 2360;
Pred. No. 12;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                .ce 1. .2360 /organism='Unclassified' /Clone='pHASE'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent: JP 1995069899-A 3 14-MAR-1995;
MITSUBISHI CHEM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCAAAAATTGAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .2360
/organism="Vaccinia virus"
/db_xref="taxon:10245"
a 410 c 399 g 693 t
                                                                                                                                                                     Orthopoxvirus.
1 (bases 1 to 2360)
Seki,M., Honda,Y. and Yamada,S.
ANTIVIRAL AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E08872
E08872.1 G1:2176976
JP 1995069899-A/4.
unidentified
unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.6 Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
JOURNAL
                                                             LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                             ORGANISM
                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
E08872
                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                   RESULT
E08871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        쉼
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
ô
                                                                                                                                                                                                                                                                                                                                                                    Vaccinia virus.
Vaccinia virus
Vaccinia virus
Vaccinia virus
Vaccinia virus
Vaccinia virus
Vaccinia virus
Orthopoxvirus.
1 (Dases I to 207)
Vasuda, K., Sato, T., Nagaya, A. and Kyo, T. action Virus
GLUCOPROTEIN, ITS PRODUCTION, RECOMBINED VACCINIA VIRUS FOR ITS
PRODUCTION, AND DIAGNOSTIC AGENT USING THE SAME
PATENT: UP 1993078395-A 6 30-MAR-1993;
NIPPON ZEON CO LID
                                                                                                                                                                                     ö
                                 'product -'fusion protein of virus protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
         CDS
                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                     29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö

    4987
    organism='Artificial sequences' FT

                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 27.8; DB 5; Length 207; Pred. No. 16; O; Mismatches 12; Indels (
                                                                                                                                                              Length 4987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48 others
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGC 51
                                                                                                                                                                                                                                                                                                       PAT
                                                                                                                                                                                        4;
                                                                                                                                                              υ
..
                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4
                                                                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 207
/organism="Vaccinia virus"
/db_xref="taxon:10245"
1 48 c 38 g 55 f
                                                                                                                                                            Query Match
41.4%; Score 28.6; D
Best Local Similarity 88.6%; Pred. No. 13;
Matches 31; Conservative 0; Mismatches
                                              fuciferase'.

Location/Qualifiers
1. 4987
Corganism="unidentified"
/db_xref="taxon:32644"
a 1041 c 1073 g 1314
                                                                                                              1314
                                                                                                                                                                                                                                                                                             DU4525 207 bp DNA
Vaccinta virus early promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.3%;
Best Local Similarity 74.5%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                            E04525.1 GI:2172726
JP 1993078395-A/6.
```

(

```
1 (bases 1 to 40)
Saitoh,S., Ohkawa,S., Saeki,S., Ohsawa,I., Funato,H., Iritani,Y.,
Sayama,S. and Takahashi,K.
Recombinant Avipox virus encoding polypeptide of mycoplasma
gallisepticum, and utilized a live vaccine
Patent: US 5871742-A 16 16-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 96)
Saitoh, S., Ohkawa, S., Saeki, S., Ohsawa, I., Funato, H., Iritani, Y., Aoyama, S. and Takahashi, K.
Aoyama, S. and Takahashi, K.
Geombinant Avipux virus encoding polypeptide of mycoplasma gallisepticum, and utilized a live vaccine
Patent: US 5871742-A 30 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999
                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                   ce 1. .38
/organism='Artificial sequences'.
Location/Qualifiers
                                                                                                                                                                                                                          Query Match 38.6%; Score 26.6; DB 5; Length 38; Best Local Similarity 87.9%; Pred. No. 32; Matches 29; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ښ
.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.3%; Score 26.4; D
83.3%; Pred. No. 38;
:ive 0; Mismatches
                                                                            1. .38
/organism="unidentified"
/db_xref="taxon:32644"
a 7 c 4 g 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AR035285 40 bp DNA
Sequence 16 from patent US 5871742.
AR035288 AR035285.1 GI:5951953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
US 5871742.
                                                                                                                                                                                                                                                                                                             5 AAAAATTGAAAAACTAGATCTATTTTTTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="unknown"
4 c 6 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR035298 96 bp
Sequence 30 from patent
AR035298
AR035298.1 GI:5951966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ပ
ထ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.3
Best Local Similarity 83.3
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
                           source
                                                                                                                                                12 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown
    FT
FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sonrce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AR035298/c
LOCUS
DEFINITION
                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                  AR035285/c
LOCUS
                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                              Luciasilieu.

E unciasilieu.

Remahashi, S., Kin, Y. and Shida, H. .

A TYPE INCLUSION (§1374/24) ATI) PROMOTER OF POXVIRUS AND EXOGENOTE EXPRESSION VECTOR COMPRISING PROPHASE PROMOTER

L Patent: JP 1994237773-A 1 30-AUG-1994;

TONEN CORP, SHIDA HISATOSHI

OS None

C Artificial sequences.

PR 1994237773-A/1

PD 30-AUG-1994

PR 22-DEC-1994

PR 22-DEC-1995 JP 937008424

PR 22-DEC-1995 JP 93700414

PR 22-DEC-1995 JP 93700414

C Strandedness: Double;

C C topology: Linear;

FR Key

Location/Qualifiers

FT SOURCE

ACGAGINESSION

ACGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 38)
Funahashi.S., Kin,Y. and Shida,H. .
Furahashi.S., Kin,Y. and Shida,H. .
A TYPE INCLUSION @(3754/24)ATI) PROMOTER OF POXVIRUS AND EXOGENOTE EXPRESSION VECTOR COMPRISING PROPHASE PROMOTER
PATENT: JP 1994237773-A 2 30-AUG-1994;
TONEN CORP, SHIDA HISATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                       29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                       PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 26.6; DE
; Pred. No. 32;
0; Mismatches
        EU/991 38 bp DNA
ATI promoter derived from Poxvirus.
E07991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU/992 38 bp DNA
ATI promoter derived from Poxvirus.
E07992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AAAAATTGAAAAACTAGTCTAATTTATTGCACG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 AAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .38
/organism="unidentified"
/db_xref="taxon:32644"
. db_ 4 c 7 g 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E07992.1 GI:2176123
JP 199423773-A/2.
unidentified.
undentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.6%;
Best Local Similarity 87.9%;
Matches 29; Conservative (
                                                                                E07991.1 GI:2176122
                                                                                                   JP 1994237773-A/1.
                                                                                                                                              unidentified
                                                                                                                                                                     unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
E07991
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                              ORGANISM
                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
E07992/c
LOCUS
                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
```

g

ď g

us-08-935-377-1.rge

```
106198 114759 contig of 7264 of in length 115260 122523 contig of 7264 of in length 123024 130348 contig of 7325 of in length 130849 130348 contig of 7325 of in length 138349 142439 contig of 7000 of in length 138240 146239 contig of 3300 of in length 146740 150037 contig of 3298 of in length 150538 153200 contig of 2663 of in length 151701 155617 contig of 1917 of in length 155118 157801 contig of 1919 of in length 15618 160479 contig of 1919 of in length 160980 162294 contig of 1919 of in length 160980 162294 contig of 1335 of in length 164849 16688 contig of 1335 of in length 16684 167879 contig of 1335 of in length 167879 contig of 1335 of in length 167879 contig of 1335 of in len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved.

14626: contig of 14626 bp in length
14627 15130: gap of
15131
30177: gap of
1504 bp
30177 30677: gap of
1501 bp
30177 30677: gap of
45326: contig of 14649 bp in length
30177 30677: gap of
45322 59056: gap of
50559 pp
59057
66714: contig of 12720 bp in length
58552 59056: gap of
67156 6714: contig of 10160 bp in length
67216 6715: gap of
77376: gap of
77376: gap of
77376: gap of
6715 6715: gap of
77376 77876: gap of
77376 77876: gap of
77376 77876: gap of
77376 77877 88354: contig of 10160 bp in length
106199 114752: contig of 7612 bp in length
106594 106198: gap of
116593: contig of 7612 bp in length
116593: contig of 7612 bp in length
116593: contig of 7321 bp in length
116593: contig of 854 bp in length
118563: 115262: gap of
118563: 1130349; gap of
118563: 1130349; gap of
11860: 137348: contig of 854 bp in length
137347: 138348: contig of 859 bp in length
137349: 138348: contig of 503 bp
14240: 145235: contig of 3296 bp in length
137340: 145235: contig of 3296 bp in length
15003: 150331: contig of 2662 bp in length
150338: 153199: contig of 2662 bp in length
150303: 15503702: gap of
15300: 15503702: gap of
155038: 153199: contig of 2662 bp in length
15503: 155035: gap of
155038: 153199: contig of 2662 bp in length
15503: 15503702: gap of
15503: 15503: contig of 2662 bp in length
15503: 15503: contig of 2662 bp in length
15503: 15503: contig of 18613 bp in length
15503: 15503: contig of 2662 bp in length
15503: contig of 18613 bp in length
15503: contig of 18613 bp in length
15503: contig of 18613 bp in length
155040: contig of 18613 bp in length
15505: contig of 18613 bp in length
15506: contig of 18613 bp in length
15507: contig of 18613 bp in length
15507: contig of 18613 bp in length
15508: contig of 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ap of 502 bp contig of 1998 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160479 160981: gap of 503 bp 160982 162383: contig of 1402 bp 162384 162894: gap of 511 bp 164342 164848: gap of 507 bp 164849 165183: contig of 147 bp 164849 165183: contig of 1835 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166184 166685; gap of 502 bp
166686 167879; contig of 1194 bp
Location/Qualifiers
1.167879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160478:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 24 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved
                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (0.3 DEC-1999) to the DDBJ/EMBL/GenBank databases. Submitted (0.3 DEC-1999) to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitsaato Univ., 1-15-1 Kitsaato, Sagamihara, Kanagawa 228-8555, Japan Kitsaato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9933, Fax:81-42-778-9924)
On Feb 18, 2000 this sequence version replaced gi:6525269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens

Bukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;

Bukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 167879)

S Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,

Ruliyama,A., Yada,T., Tochoki,Y., Watanabe,H. and Sakaki,Y.

Homo sapiens 167,879 genomic DNA of 11q14

L Published Only in DataBase (1999) in press

E 2 (bases 1 to 167879)

S Hattori,M., 1911,K., Totoda,A., Taylor,T.D., Hong-Seog,P.,

Fullyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AP000827 167879 bp DNA HTG 04-FEB-2000
Homo sapiens chromosome 11 clone RP11-716D19 map 11q14, WORKING
DRAFT SEQUENCE, 24 unordered pieces.
AP000827
AP000827.1 GI:6997662
                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://hgp.gsc.riken.go.jp/
Contact: hattorl@gsc.riken.go.jp/
Contact: hattorl@gsc.riken.go.jp/
Contact: hattorl@gsc.riken.go.jp/
Contact: hattorl@gsc.riken.go.jp/
Center project name: Humbraftll
Center project name: RP11-716D19
Center clone name: RP11-716D19
Center clone name: RP11-716D19
Center clone name: RP11-716D19
Center clone name: RP11-716D19
Consensus quality: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 140881 bases at least Q40
Consensus quality: 140882 bases at least Q40
Consensus quality: 154204 bases at least Q20
Consensus quality: 154204 bases at least Q20
Consensus quality: 154204 bases at least Q20
Consensus quality: 134204 bases at least Q20
Losert size: 156754; sum-of-contigs
Quality coverage: 156754; sum-of-contigs
                                                                                                                                                                                                          ö
                                                                                                                     Length 96,
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14626 of 15050 of 14650 of 12730 of 7659 of 10479 of 7619 of 7619 of 8723 of
                                                                                                                                                                                                          9
                                                                                                                         DB 5;
                                                                                                                                                                                                                                                                                   5 AAAAATTGAAAAACTAGATCTATTTTATTGCACGCGG 40
                                                                                                                             Score 26.4; DB; Pred. No. 43; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-716D19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14626 contig of
30176 contig of
45326 contig of
58556 contig of
66715 contig of
77376 contig of
96474 contig of
105697 contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: RIKEN
                                                                                                                                 Query Match 38.3%;
Best Local Similarity 83.3%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15127
30677
45827
59057
67216
77877
88856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
AP000827/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
```

Gaps

ö

67

ò

```
/codoo_start=1
//transl_table=11
/protein_id="BAA22407.1"
/brotein_id="BAA22407.1"
/db_xref="G1:2443.08"
/translation="MSAEAFODDADIQLFAEERAAVADAVPRRRREFSTVRRCARAAL
GELGIPPPVLPGGRHRAPOWPTGVVGSWTHCGGYRAAAVARASRLHSVGIDAEESAPL
PDGVLDLVGLPXERDOVERLGAGSDAVPWDRLLFSCREAVXKWFPLAQRLLGFDGAR
IDIDSGGFFSARFLVPPPLASGNPVPRLTGRWMHRDGLLLTAALALPGFLGFDGAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC016688 186326 bp DNA HTG 31-JAN-2000
Homo sapiens clone RP11-80J14, WORKING DRAFT SEQUENCE, 20 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Jan 31, 2000 this sequence version replaced gi:6524391.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 186326)
Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                6 others
                                                                                                                                                                                                                                                                                                                                                                         18 CTAGATCTATTTGCACGCGCCGCCATGGGCCCGGCCGCCAACGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site:http://genome.wustl.edu/gsc/index.shtml
                     /note="unnamed protein product"
                                                                                                                                                                                                         464 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC016688
AC016688.2 GI:6838910
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                    945 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 186326)
Waterston, R.H.
                                                                                                                                                                                                      o 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WUGSC
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                         ៧
                                                                                                                                                                                                         486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
AC016688/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="mrshilgrieldoerlgrdleyuatvptveeevdefsngewkni
Plytransgesdriktrolegspa.pptkhaeovpytknei itttvugerlomartrnlkna
vviphroefveldreidotftkthuledsplafhsdodtvihmrageimfloaavhsa
vnfaresroslcvolafbgardekbafadatvyaphilspuvrerkrerbasilal
sgvigrenerdilflensvhytydvhpgetfemleni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (17-SEP-1997) to the DDBJ/EMBL/GenBank databases. Takeshi
Shibasaki, Kyowa Hakko Kogyo Co., Ltd., Tokyo Research Laboratory;
3-5-6 Asahimachi, Machida, Tokyo 194, Japan (Tel:0427-25-2555,
Fax:0427-26-8330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="Baa22405.1"
/db_xref="GI:2443306"
/translation="MQPLGDHAPDPDGDLPAELGVLCAQLPHGSGVELPXPHRAHRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGLVGDLTGEAHQPFAVHGLKSRGHGGDGGHRTGSLHGFCSQRGRTPLGAPRATRARP
GGFRPHQVGRVALRSTSGALRIPSPPPPRDSFRLNNPPARRQETVDCODAAKLGSIFEC
GSELGSCSAATEGDWGDLPFAECRRPEHAHRVCLGFFVMSDHRPFSGRLLRVHLTFGY
                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQVIEVRREVPGPADQFIVIERLDDGGPAAGHVOVEGDGTGAQDPEAVGAPPLLEQAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 2900)
Shibasaki,T.
                                                                                                                                                                                                                                                                                                                                                                                            DNA BCT 27-SEP-1997
L-proline 3-hydroxylase, complete cds.
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mori, H., Shibasaki, T., Yano, K. and Ozaki, A.

Purification and cloning of a proline 3-hydroxylase, a novel
which hydroxylates free L.proline to cis-3-hydroxy-L.proline
J. Bacteriol. 179 (18), 5677-5683 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On Sep 27, 1997 this sequence version replaced g1:1747311.
D78337: submitted (17-Nov-1995).
                                                                                                                                                                Length 167879,
                                                                                                                                                                                                      ö
                 /chromosome="11"
/clone="RP11-716D19"
/map="11q14"
1 28817 c 28130 g 48047 t 13675 others
                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AB007189.1 GI:2443305
L-proline 3-hydroxylase.
Streptomyces sp. (isolate:TH1) DNA, clone:pTH30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="L-proline 3-hydroxylase"
/protein_id="BAA22406.1"
/db_xref="G1:2443307"
                                                                                                                                                             Score 26.2; DB 32;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297. .1208
/note-"unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces sp."
/isolate="TH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLLALALPVAILDASHRECGGDSRLPR'
                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                   DD 74276 GGCTAAAATTGCAAAACTAGATCTATTTGT 74246
                                                                                                                                                                                                                                             31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1931"
/clone="pTH30"
'db_xref-"taxon:9606"
                                                                                                                                                                                                                                                GGCCAAAATTGAAAAACTAGATCTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .2900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                          AB007189 2900 bp D. Streptomyces sp. DNA for AB007189 D78337 AB007189.1 GI:2443305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GARALGERFSLTTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                           ch 38.0%;
1 Similarity 90.3%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1312. .2184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces sp
                                                                             49210 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (sites)
                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                   RESULT
AB007189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
```

```
Saeki, S., Ohsawa, I., Funato, H., Iritani, Y.,
             Saeki, S., Ohsawa, I., Funato, H., Iritani, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 97)
Sabitohs., Ohkawa, S., Saeki, S., Ohsawa, I., Funato, H., Iritar Satich, S., and Takahashi, K.
Recombinant Avipox virus encoding polypeptide of mycoplasma gallisepticum, and utilized a live vaccine
Patent: US 58/1742-A 27 16-FEB-1999;
Location/Qualifiers
1 (bases 1 to 93)
Saltoh,S., Ohkawa,S., Saeki,S., Ohsawa,I., Funato,H., Iritan
Aoyana,S. and Takahashi,K.
Recombinant Avipox virus encoding polypeptide of mycoplasma
gallisepticum, and utilized a live vaccine
Patent: US 58/1742-A 28 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 97;
                                                                                                                                                                                                                                     Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1997 (Rel. 52, Created)
08-OCT-1997 (Rel. 52, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97
                                                                                                                                                                                                                                                                                                            5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGGC 41
                                                                                                                                                                                                                                                                                                                                 Score 25.8; DE
Pred. No. 69;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AAAAATTGAAAAACTATTCTAATTTATTGCACTCGTC
                                                                                                                                                                                                                                    37.4%; Score 25.8; Dilarity 81.1%; Pred. No. 69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44
                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA
US 5871742.
                                                                                                                                                                 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; DNA; UNC; 36 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unknown"
11 c 8 g
                                                                                                                                              /organism="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic early promoter sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          AR035295 97 bp
Sequence 27 from patent
AR035295 GI:5951963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.4%;
milarity 81.1%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 30; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
Unclassified.
                                                                                                                                                                                                                                                 Local Similarity
les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP 1996242869-A/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34 a
                                                                                                                                                                     ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E12061.1
                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E12061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E12061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
E12061
                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
AR035295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                               Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAA 62
     soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26; DB 52; Length 186326;
Pred. No. 1.7e+02;
0; Mismatches 25; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 17057 bp in length
gap of unknown length
gap of unknown length
contig of 22244 bp in length
gap of unknown length
contig of 37678 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      f unknown length
g of 9468 bp in length
f unknown length
of 7975 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
of 13804 bp in length
unknown length
of 18625 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                             of 10085 bp in length
unknown length
of 8661 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                          bp in length
length
bp in length
                                                                                                                                                                                                                                                                                                    length
                                                                                                                 bp in length
length
                                                                                                                                                      of 1704 bp in length
unknown length
of 1150 bp in length
                                                                                                                                                                                                                                                                   of 2644 bp in length
                                                                                                                                                                                                                                                                                                                       unknown length
of 3690 bp in length
                                                                                                                                                                                                                                                                                                                                                                              of 7462 bp in length
                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAT
                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                    ength.
                                                                                                     ength
                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 13094 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 186326
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-80714"
a 40241 c 39737 g 52239 t
                                                                                                 gap of unknown I contig of 2573 begond to 1704 begond of 1704 begap of unknown I contig of 1150 begap of unknown I contig of 1856 begap of unknown I contig of 1856 contig of 2644 begap of unknown I contig of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR035296 93 bp DNA
Sequence 28 from patent US 5871742.
AR035296
                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                              contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AR035296.1 GI:5951964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.78;
62.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63824:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76918:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90722:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109347:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126404:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148648:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186326:
                                                                                                                                                                                                                                10354:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        46381:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55849:
                                                                                                                                                                                               8398:
                                                                                                                                                                                                                                                                                                                                                                                                                   37720:
                                                                                                                        5544:
                                                                                                                                                           7248:
                                                                                                                                                                                                                                                                                                        16483:
                                                                                                                                                                                                                                                                                                                                           20173:
                                                                                                                                                                                                                                                                                                                                                                                27635:
                                                                                                                                                                                                                                                                     12998:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62.1*
....nes 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
Unknown.
Unclassified.
                             preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126405
                                                                                                                      2972
                                                                                                                                                             5545
                                                                                                                                                                                               7249
                                                                                                                                                                                                                                    8399
                                                                                                                                                                                                                                                                     10355
                                                                                                                                                                                                                                                                                                          12999
                                                                                                                                                                                                                                                                                                                                                                                20174
                                                                                                                                                                                                                                                                                                                                                                                                                     27636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54067 a
                                                                                   1457
                                                                                                                                                                                                                                                                                                                                               16484
                                                                                                                                                                                                                                                                                                                                                                                                                                                          37721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5510 GGGCCG 5505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 000000 68
```

source

FEATURES

BASE COUNT ORIGIN

셤 ö

ö

ö

RESULT 11
AR035296/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

29-SEP-1997

PAT

ė

ż

```
Tables 1 to 40)
Yamaquchi,T., Fukushi,H., Hirai,K., Aoyama,S., Yamaquchi,T.,
Iritani,K., Hayashi,Y., Ogawa,R., Takamura,C. and Kamoqawa,K. .
PROMOTER FOR COMBINED POXVIRUS AND RECOMBINENT POXVIRUS HAVING THE
Patent: JP 1995067655-A 1 14-MAR-1995;
NIPPON ZEON CO LTD, SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAKAMURA CHIZUKO, KAMOGAWA KOICHI
C12N15/09,A61K39/275,C12N7/00,(C12N15/09,C12R1:92),(C12N7/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YAMAGUCHI TAKESHI, IRITANI KOICHI, HAYASHI YUKIHIRO, PI
                                                                                                                                                                                                                                                                                                                                                                                           Artificial sequences.
JP 1995067655-A/1
14-MAR-1993
30-AUG-1993 JP 1993238953
YAMAGUCHI TAKESHI, FUKUSHI HIDETO, HIRAI KATSUYA, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .40
/organism="unidentified"
/db_xref="taxon:32644"
a 7 c 5 g 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12R1:92);
strandedness: Double;
                                                              E08848 40 bp I Poxvirus early promoter. E08848 E08848.1 GI:2176952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        topology: Linear;
                                                                                                                                                     JP 1995C67655-A/1.
unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ಥ
                                                                                                                                                                                                                                                                                                                                                                               None
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIGEMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PI YZ
OGAWA 1
DO CAWA 1
DO CC CC CC CC CC CC FFH KG FFH KG FFT SC FFT SC
                                                                                     DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                       KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                             TITLE
                      RESULT
E08848
                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 40)
Saltoh,S., Ohkawa,S., Saeki,S., Ohsawa,I., Funato,H., Iritani,Y.,
Aoyama,S. and Takahashi,R.
Aoyama,S. and Takahashi,R.
Geombinant Avipox virus encoding polypeptide of mycoplasma
gallisepticum, and utilized a live vaccine
Patent: US 5871742-A 15 16-FEB-1999;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Length 40;
                                                                                                                                                   Artificial sequences.
JP 1996242869-A/2
24-28P-1996
16-JAN-1996 JP 1996023125
13-JAN-1995 JP 95P 21249
KAMOGANA KOICHI, OGAWA RYOHEI, YAMAGUCHI TAKESHI, HIRAI KATSUYA C12N15/09, A61K39/12,C12N7/00; strandedness: Double; topology: Linear; hypothetical: No; anti-sense: No;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
1-36
Kamogawa K., Ogawa R., Yamaguchi T., Hirai K.;
RECOMBINANT POXVIRUS AND VACCINE COMPRISING THE SAME";
Patent number JP 1996242869-A/2, 24-SEP-1996.
NIPPON ZEON CO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Artificial sequences"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 36 BP; 15 A; 5 C; 3 G; 13 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AAAAATTGAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.8%; Score 25.4; D
Best Local Similarity 82.9%; Pred. No. 82;
Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25.4; D
Pred. No. 84;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AR035284 40 bp DNA
Sequence 15 from patent US 5871742.
AR035284 1 GI:5951952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13
                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"unidentified"

    .36
    /db_xref="taxon:32644"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unknown"
7 c 5 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 36.8%;
Best Local Similarity 82.9%;
Matches 29; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unknown.
Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
AR035284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                   SOURCE
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

.40
 /organism='Artificial sequences'.

13

Location/Qualifiers

AOYAMA

ö Gaps ö Length 40; Indels 9 DB 5; 6 AAAAATTGAAAAACTATTCTAATTTATTGCACTCG 40 5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCG 39 Query Match 36.8%; Score 25.4; D Best Local Similarity 82.9%; Pred. No. 84; Matches 29; Conservative 0; Mismatches Search completed: May 29, 2000, 21:33:53 Job time: 36765 sec

4 .7 .215

**5**,

```
Result
                                                       May 29, 2000, 17:05:30 ; Search time 2276.24 Seconds (without alignments) 135.250 Million cell updates/sec
                                                                                                                  1 GGCCAAAATTGAAAACTA......GCCCGGCCGCCAACGGCGGA 69
                                                                                                                                                                                                                                                              /cgn1_6/ptodata/1/pna/US091C_COMB.seq
/cgn1_6/ptodata/1/pna/US092A_COMB.seq
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                   5142629 segs, 2230885800 residues
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     - nucleic search, using sw model
                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                             US-08-935-377-1
69
                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn1_t
                                                                                                          Perfect score:
                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                             ..
                                       OM nucleic
                                                                                                                  Sequence:
                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                             Database
                                                          Run on:
```

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
          cgn1_6/ptodata/1/pna/US0922_COMB.seq:*

cgn1_6/ptodata/1/pna/US0922_COMB.seq:*

cgn1_6/ptodata/1/pna/US0922_COMB.seq:*

cgn1_6/ptodata/1/pna/US0922_COMB.seq:*

cgn1_6/ptodata/1/pna/US0932_COMB.seq:*

cgn1_6/ptodata/1/pna/US0932_COMB.seq:*

cgn1_6/ptodata/1/pna/US0932_COMB.seq:*

cgn1_6/ptodata/1/pna/US094A_COMB.seq:*

cgn1_6/ptodata/1/pna/US094A_COMB.seq:*

cgn1_6/ptodata/1/pna/US094A_COMB.seq:*

cgn1_6/ptodata/1/pna/US094A_COMB.seq:*

cgn1_6/ptodata/1/pna/US094A_COMB.seq:*

cgn1_6/ptodata/1/pna/US094A_COMB.seq:*

cgn1_6/ptodata/1/pna/US001A_COMB.seq:*

cgn1_6/ptodata/1/pna/US6001A_COMB.seq:*

cgn1_6/pto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgnl_6/ptodata/1/pna/US07_NEW_COMB.seq
/cgnl_6/ptodata/1/pna/US08_USWB_COMB.seq
/cgnl_6/ptodata/1/pna/US09_NEW_COMB.seq
/cgnl_6/ptodata/1/pna/US00_NEW_COMB.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        % .
Ouerv .
```

Description	Sequence 1, Appl1 Sequence 5, Appl1
uic No. Score Match Length DB ID	69 28 US-08-935-377-1 57 28 US-08-935-377-5
8	28
Length	69
Match 1	69 100.0 57 82.6
No. Score Match Length DB ID	69
NO.	77

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                           Sequence 7, Appli
Sequence 8, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 31, Appl
Sequence 27, Appl
Sequence 406, Appl
Sequence 409, Appl
Sequence 409, Appl
Sequence 409, Appl
Sequence 410, Appl
Sequence 410, Appl
Sequence 410, Appl
Sequence 410, Appl
Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 5, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08935377
Sequence 1, Application US/08935377
GENERAL INFORMATION:
TILLE OF INVENTION: T Cells Specific for Target Antigens and TILLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D. C.
COUWTY: USA
IP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
8 US-08-935-377-23

8 US-08-935-377-24

8 US-08-935-377-6

8 US-08-935-377-6

8 US-08-935-377-9

8 US-08-935-377-9

8 US-08-935-377-3

8 US-08-935-377-3

8 US-08-935-377-3

10 US-08-935-309A-406

10 US-08-932-610-409

10 US-08-932-610-410

10 US-08-933-3

10 US-08-133-3

10 US-08-133-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1341
47677
14103
40
40
101
678
7206
870
870
870
1081
1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-08-935-377-1
                                                                                                                                                                                                                                        0000
```

ATTORNEY/AGENT INFORMATION:

CLASSIFICATION:

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGCCAAAAATTGAAAAACTAGATCTATTATTGCACGCGGCGGCCGCCATGGGCCCGGCCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-09-935-377-5
US-09-935-377-5
Sequence 5, Application US/08935377
Sequence 5, Application US/08935377
SENERAL INFORMATION:
TITLE OF INVENTION: T Cells Specific for Target Antigens and TITLE OF INVENTION: T Cells Specific for Target Antigens and TITLE OF INVENTION: T Cells Specific for Target Antigens and TITLE OF INVENTION: T Cells Specific for Target Antigens and TITLE OF INVENTION: T CELLS SPECIFIC STATES: 37
CORRESPONDENCE: Sterne, Kessler, Goldstein & Fox P.L.L.C STARE: D. C.
STATE: D. C.
COUNTRY: USA
ZIP: 20005
COMPUTER: NEADABLE FORM:
COMPUTER: IBM PC Compatible
COMPUTER: D. D. C.
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE FORM:
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 69; DB 28; Length 6

Best Local Similarity 100.0%; Pred. No. 5.2e-15;

Matches 69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET UNMBER: 36,688
REGISTRATION NUMBER: 36,688
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 371-2600
INFORMATION FOR SEQ ID NO: 5:
SEGURENCE CHARACTERISTICS:
LENDING CHARACTERISTICS:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
INFORMATION FOR SED ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 69 Dase pairs
ITYPE: nucleic acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACGGCGGA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: CDS
; LOCATION: 46..
US-08-935-377-1
```

```
; MOLECULE TYPE: CDNA
US-08-935-377-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                 Gaps
                                                                                              1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCC 57
                                                 ö
                                                                                                                          1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                    Sequence 23, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDED: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STRYE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 3
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 82.6%; Score 57; DB 28; Length 57; Best Local Similarity 100.0%; Pred. No. 9.8e-11; Matches 57; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 76.8%; Score 53; DB 28; Length 53
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 53; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 2005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SUFTAME: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 42-SEP-1997
CLASSIFICATION: 42-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFERENCE/POCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELEFAN: (202) 371-2540
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
US-08-935-377-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-08-935-377-24/c
                                                                                                                                                                                                                                        US-08-935-377-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                 ò
                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
```

State of the B

```
COMPATION WINDER: PROPER disk
COMPATINE IN COMPATINE
COMPATINE IN COMPATINE
```

```
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Inear MOLECULE TYPE: CDNA US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                         ö
                                                                                                                                                                 1 GGCCAAAAATTGAAAAACTAGATCTATTATTGCACGCGGCGCCCCATGGGCCCGGCC 60
                                                                                                                                                                                                        1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCGGTGGATCCCCCGGGC 60
                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                     US-08-935-377-7

US-08-935-377-7

Sequence 7, Application US/08935377

GENERAL INFORMATION:

APPLICANT ZAUGETE, Maurice

TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zauderer, Maurice
IITLE OF INVENTION: T Cells Specific for Target Antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 148;
                                                                              DB 28; Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGCCAAAATTGAAAACTAGATCTATTTATTGCACGCGGCCGCCATGG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGG 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALUNESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, N.W., Sulte 600 CITY: Washington STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATEMIN PC-DOS/MS-DOS
SOFTWARE: PATEMIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 71.0%; Score 49; DB 28; I Best Local Similarity 100.0%; Pred. No. 9.6e-08; Matches 49; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1821.0010000/EKS/CMB
                                                                                Score 49; DB 28;
Pred. No. 9.5e-08;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
                                                                                Query Match 71.0%;
Best Local Similarity 84.6%;
Matches 55; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: CDNA US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D. C. COUNTRY: USA
; MOLECULE TYPE:
US-08-935-377-6
                                                                                                                                                                                                                                                           61 AACGG 65
                                                                                                                                                                                                                                                                                                    61 TGCAG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                             ò
                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                      ద
```

```
NUMBER OF SECURATION VACCINES Based Thereon
NUMBER OF SECURENCES: 17
CORRESPONDERSER: Sterme Kessis: Coldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITTY: Washington
CITY: Washington
COUNTY: USA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COUNTY: USA
COUNTY: TREE : THE PROCESSIS: 180
CONSTINE: 180
CONS
```

```
Query Match
Best Local Similarity 100.
Matches 36; Conservative
                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   55 GCCGCCAACGGCGGA 69
                                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lirear
                                                                                                                                                                                                                                                                             CITY: Washing
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE:
US-08-935-377-30
                                                                                                                                                                                                                                                                                                                                  20005
                                                                                         RESULT 10
US-08-935-377-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                             g
     ò
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCCAAAAATTGAAAACTAGATCTATTTATTG-----CACGCGGCCGCCATGGGCCCG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 28; Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 28; Length 75
Pred. No. 0.0016;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                    1 GCCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATG 48
                                                                                                                                                                                                                                                                                                    ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: D. C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
ATONNEY/AGENT INFORMATION:
NAME: SCAFÍE, ELIC K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET UNBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10FPRATION:
TELECOMMUNICATION 10FPRATION:
TELECOMMUNICATION 10FPRATION:
TELEFRAX: (202) 371-2560
INFORMATION FOR SEO ID NO: 3:
SEGUENCE CHRARCTERISTICS:
FUNDAMET TO SEE PAILS
                                                                                                                                                                                                                DB 28; L
                                                                                                                                                                                                                69.6%; Score 48; DB illarity 100.0%; Pred. No. 2.2 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.68;
78.78;
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDENNESS: single
   (202) 371-2600
                                        <u>ه</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 78.7
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
52..75
                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                          TOPOLOGY: 11r

MOLECULE TYPE:

US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-935-377-3
                                                                                                                                                                                                                                                                                                                                                                                         US-08-935-377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ð
                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
RESULT 10

Sequence 11

Sequence 12

Sequence 12

SEQUENCES 12

SEQUENCES 13

SEQUENCES 13

SEQUENCES 13

SEQUENCES 13

SEQUENCES 13

SEQUENCES 13

SEGUENCES 14

SEGUENCES 14

SEGUENCES 15

SEGUENCE
```

```
Gaps
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                Sequence 406, Application US/08592610
GENERAL INFORMATION:
APPLICANT: MAKOLO SEKI et al.
TITLE OF INVENTION: ANTISENSE COMPOUNDS COMPLEMENTARY TO HCV
TITLE OF INVENTION: GENOME
NUMBER OF SEQUENCES: 410
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MAKOTO SEKI et al.
TITLE OF INVENTION: ANTISENSE COMPOUNDS COMPLEMENTARY TO HCV
TITLE OF INVENTION: GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 40;
                                                                                                            Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , DB 17;
1.3;
                                                                                                               Score 28.6; DB 12;
Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other nucleic acid, synthetic DNA US-08-592-610-406
                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ...
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
~~wbuter: IBM Compatible
~~wbuter: IBM Compatible
~~wstem: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41.4%; Score 28.6; D
88.6%; Pred. No. 1.3;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CCAAAAATTGAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 CCAAAATTGAAAACTAGTCTAATTTATTGCACG 38
                                                                                                                                                                                                                       3 CCAAAAATTGAAAAACTAGATCTATTTATTGCACG 37
                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/592,610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-295-309A-406
; Sequence 406, Application US/09295309A
; GENERAL INFORMATION:
; APPLICANT: Makoto SEKI et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/111,465
FILING DATE: August 25, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Matthew Jacob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 25,154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                               41.4%;
                                                                                                               Query Match
Best Local Similarity 88.65
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.6
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 805 Fire CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                      RESULT 13
US-08-592-610-406
                                                     US-08-301-013-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 46.4%; Score 32; DB 28; Length 71; Best Local Similarity 100.0%; Pred. No. 0.095; Matches 32; Conservative 0; Mismatches 0; Indels
SOFTWARE: PC-DOS/MS-DOS
SUFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
ATONREY/AGENT THE AND ADDRESSIFICATION: A24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other nucleic acid synthetic DNA
                                                                                                                                                                                                                                          1821.0010000/EKS/CMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Makoto SEKI et al.
APPLICANT: Makoto SEKI et al.
TITLE OF INVENTION: ANTIVIRAL AGENT
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AAAAATTGAAAAACTAGATCTATTTATTGCAC 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/301,013
FILING DATE: September 6, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/299,113
FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-260
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08301013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA US-08-935-377-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27, Applicat
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-301-013-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

Gaps

ô

Length 234;

```
5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGCCGCCATGGGCCCGG
                                                                                                                                                                                                                                                                         Query Match
41.4%; Score 28.6; DB
Best Local Similarity 72.5%; Pred. No. 2.2;
Matches 37; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: May 30, 2000, 09:48:19 Job time: 60169 sec
APPLICATION NUMBER: US 07/750, FILING DATE: 26-AGC-1991
ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERNCE/DOCKET NUMBER: 30472 TELEPHONE: (202)672-5399 TELEX: 904136 FOR EEQ ID NO: 89: SEQUENCE CHARACTERISTICS: LENGTH: 234 base pairs TYPE: nucleic acid STRANDENESS: single
                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 89, Application US/08358928
GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: SCHEIFLINGER, Michael
TITLE OF INVENTION: UTRUSES CONTAINING HUMAN IMMUNOBECIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other nucleic acid, synthetic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                  2: Wenderoth, Lind & Ponack, L.L.P.
2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
41.4%; Score 28.6; Di
Best Local Similarity 88.6%; Pred. No. 1.3;
Matches 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CCAAAAATIGAAAAACTAGATCTATTTATIGCACG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
                             CITY: Washington
STATE: District of Columbia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-295-309A-406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-358-928-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

**ì**,

OM nucleic

Run on:

```
9D_est25:..
9D_est26:..
9D_est28:..
9D_est28:..
9D_est28:..
9D_est28:..
9D_est31:..
9D_est31:..
9D_est32:..
9D_est33:..
9D_est33:..
9D_est33:..
9D_est33:..
9D_est33:..
9D_est33:..
9D_est33:..
9D_est33:..
                                                                                                                                                                                                                                                                                                                                                                   em_est29:*

qb_est40:*

qb_est41:*

qb_est41:*

qb_est41:*

em_est31:*

em_est33:*

em_est33:*

em_est33:*

em_est41:*

em_est33:*

em_est
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    998:
1000:
1001:
1005:
1006:
1008:
1008:
 May 29, 2000, 11:04:41; Search time 2192.43 Seconds (without alignments) 127.563 Million cell updates/sec
                                                                                                                                                                       US-08-935-377-1
69
1 GGCCAAAAATTGAAAAACTA......GCCCGGCCGCCAACGGCGGA 69
                                                                                                                                                                                                                                                                                                                     9714632
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                     4857316 seqs, 2026611650 residues
                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - nucleic search, using sw model
                                                                                                                                                                                                                                       IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_est14:*
em_est15:*
em_est16:*
em_est17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est9:.*
gb_est10:.*
gb_est11:.*
gb_est11:.*
gb_est14:.*
gb_est15:.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_est18:*
em_est19:*
gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est17:*
gb_est18:*
gb_est19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est21:*
gb_est22:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             em_est10:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_est12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_est11:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est20:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_est13:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9b_est3.
9b_est4....
9b_est4...
9b_est5...
9b_est6...
                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_est1::
em_est2::
em_est3::
em_est4::
em_est4::
em_est5::
em_est6::
em_est8::
em_est8::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                        Scoring table:
```

Database :

Searched:

Sequence:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_gss12:*
gb_gss13:*
gb_gss14:*
gb_gss14:*
gb_gss15:*

em_gss11:* em_gss12:*

em_gss9:* em_gss10:*

em_gss8:* gb_gss11:* gb_gss10:*

em_gss7:*

em_gss2: *
em_gss3: *
em_gss3: *
em_gss5: *
em_gss5: *
em_gss5: *
em_gss5: *
em_gss5: *
em_gss7: *
em_gss7: *
em_gss8: *

SUMMARIES

Suzuk Tsunc Vokot	TITLE RICED TOURNAL Unput CONTENT CONT	Polyy Toman Toman Toman Okazz Okaz Oka	BASE COUNT ORIGIN Query Match Best Local Sim Matches 36; Qy 1 GGCCAAL                   Db 68 GGCCAAL
Description	AV281309 AV281309 AA60654 vm93a06.r AQ274419 mgxb0015M AL106287 DrCscophil AQ406794 HS_5103_B AQ412765 HS_5160_B AQ415765 HS_5160_B AQ415486 RPC1-11-1 AQ381488 RPC11-11-1 AQ381488 RPC111-12 AW25566 xq60903.x AW25566 xq60903.x AW26566 xq60903.x AW36484 32589 MAR AQ064961 HS_222_B AQ339014 ES_244246 AQ139014 ES_244246	AW143615 EST293911 AQ328078 mgxx0010E T62402 TGEST293911 AA012360 TGEST2798h0 AA011912 TGEST2798h0 AA011912 TGEST2798h0 AA011912 TGEST2798h0 AA011912 TGEST2798h0 AA011912 TGEST2798h0 AA011913 TGEST279810E N60106 TGEST27910E1 N60192 TGEST27910E1 AA519942 TGEST2793E1 AA519942 TGEST2769 AA71942 TGEST2769 AA71942 TGEST2769 AA71947 TGEST269 AA729295 TAS56110.8 AA443577 ZW35801.8 AA443577 ZW35801.8 AA729295 TAS5610.8 AA729295 TAS5610.8 AA729295 TAS5610.8 AA729295 TAS5610.8 AA73612 TGEST32803.X AA73612 TGEST322A	ALIGNMENTS  AV281309
a	AV281309 AA606654 AA606654 AA606654 AA4196 AA412486 AA212765 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486 AA415486	AW143615 T6AC98078 T6AC98078 AA012360 W95580 MA012016 W00132 W00131 W00133 M6068 N60068 N60068 N60068 N60068 AA219942 AA220329 AA220329 AA220329 AA319942 AA319942 AA319942 AA319942 AA31944871 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA31826 AA3182	ALIGNMENTS  223 bp mRNA full-length enriched, clone 4933423P14 3', ml  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269346  1:6269
DB I	711 361 105 106 106 106 729 729 732	C	Dp 11-1e ne 49 69346 69346 69346 8933 33) 831, Y 811, Y 81
Query Match Length I	464 464 464 1201 1201 492 603 603 630 630 630 630 630 630 630 8379 194 278 849	0.000	AV281309 223 bp AV281309 RIKEN full-le musculus cDNA clone 49 AV281309 GI:6269346 EST. house mouse. house musculus Eukaryota; Metazoa; Ch Eutheria; Rodentia; Sc I (bases 1 to 223) Konno,H., Aizawa,F., A Fukuda,S., Fukunishi,Y Euhi,Y., Ishiwan,T., Kai,C., Kawal,J.; Kiku Matsuyama,T., Miki,R., Matsuyama,T., Miki,R., Matsuyama,T., Miki,R., Ova,C., Ozawa,Y., Sait
Query	1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		AV281309 AV281309 RI AW281309 I AV281309 I EST. EST. EST. EVERTYOLA; ELHEATA; RI L (Dases I L (Dases I L (Ases I L (Ases I) L (Ases
Score	25.6 6 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	24400000000000000000000000000000000000	
Result No.	00 00 00 00 00 00 00 00 00 00 00 00 00	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 LOCUS LOCUS DEFINITION ACCESION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS

6

```
/tissue_type="testis"
/dev_stage="adult"
/dev_stage="adult"
/lote="site_1: Sall; Site_2: BamHI; cDNA library was
/note="site_1: Site_1: Site_1: Sall; Sall; Site_1: Site_1: Site_1: Site_1: Sall; Site_1: Sit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M. Kitsunai.T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Carahinci.P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y. Ozawa,Y., Muramatsu,M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci.P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer adapter of sequence [57] primer adapter of sequence [57] convacages and sequence [57] convacages and sequence [58] convacages and sequence and sequence and sequence and sequence sequence and sequence seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
uki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Inoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Octa, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. CEN Mouse ESTS (Konno, H., et al.)

Jul 9, 1999 this sequence version replaced gi:5434327.

Tutact: Yoshihide Hayashizaki

Tome Exploration Research Group, Life Science Tsukuba Center, once Exploration Research Group, Life Science Laboratory

Institute of Physical and Chemical Research (RIKEN), Genomic ences Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RIKEN full-length enriched, adult male testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     i1: genome-res@rtc.riken.go.jp,
:http://genome.rtc.riken.go.jp/
aki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
suura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
ashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGC 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 27; DB 71; Length 223;
Pred. No. 60;
0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
: +81-298-36-9013
: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="4933423P14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.1%;
illarity 70.6%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 milarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65
```

LOCUS AA606654/c

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

ACCESSION VERSION KEYWORDS SOURCE

```
/db_xref="tcaxon:89476"
/clone="mqxb015M12r"
/clone="mqxb015M12r"
/clone="mqxb015M12r"
/clone="mqxb015M12r"
/closue_type="Tcotollasts"
/lab_host="E. coli DH10B"
/note="vector: pBACWICH; Site_l: HindIII; Site_2: HindIII;
/note="vector: pBACWICH; Site_l: Site_a hindIII;
/note="vector: page: not page: not for sudding a haploid genome (n=7) of approximately 40 Mbp. Rice
/nomerous aspects of the fungal-host interaction. In
/nomerous aspects of the fungal-host interaction. In
/note="vector: note; page: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration of this BAC-end sequence will be sequence to a part of this Lucopean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
                                                                     1 (bases 1 to 692)
Yu.Y., Zhu.H., Boyd.C.A., Gaudette,B., Gayle,A., Kingsbury,R.,
Phillips K., Sasinowski,M. Wing.R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence SP6 end of BAC BACNISC21 of DrosBAC library from Drosophila melanogaster (fruit ALI), genomic survey sequence.
                                  Eukaryota; Fungi; Ascomycota; anamorphic Ascomycota; Pyricularia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                              Contact: Dean RA
Clemson University Genomics Institute
Clemson University
Clemson University
Tel: 864 656 5737
Fax: 864 656 4293
Email: rdean@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 37.4%; Score 25.8; DB 105; Similarity 67.9%; Pred. No. 1.3e+02; 36; Conservative 0; Mismatches 17; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Pyricularia grisea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 390.
Location/Qualifiers
1. .692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="70-15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL106287.1 GI:5621177
                                                                                                                                                                                                                                                                                Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                             Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                     REFERENCE
                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 464)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Morre,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ274419 692 bp DNA GSS 03-NOV-1998 mgxb0015M12r CUGI Rice Blast BAC Library Pyricularia grisea genomic clone mgxb0015M12r, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
AAGO6654 464 bp mRNA EST 30-SEP-1997 vm93a06.rl Knowles Solter mouse blastocyst B1 Mus musculus CDNA clone IMAGE:1005778 5' similar to gb:L33715 Mus musculus Fau gene, AAGO6654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Many many mode of the control of control of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 GGCACAACATIGACAAAGCGCCGGTITITACTGCATICGGCCTTCTIGGCCCCGGCC 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="B6D2 F1/J"
/db_xref="taxon:10090"
/clone="IMAGE:1005778"
/clone="IMAGE:1005778"
/clone="IMAGE:1005778"
/clone="IMAGE:1005778"
/clone="IMAGE:1005778"
/clone="IMAGE:1005778"
/clone="IMAGE:1005778"
/de_stage="blastocyst"
/de_stage="embryo (pre-implantation)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGCCAAAAATTGAAAAACTAGATGTATTTATTGCACGCGGCCGCCATGGGCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 26.6; 1
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vector to vector length is 491.
Location/Qualiflers
1. 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inserts) and B3.
131 c 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative full length read
                                                                                                                                                                                                                                                                            AA606654.1 GI:2455588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ274419.1 GI:3827734 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.68;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyricularia grisea.
Pyricularia grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 66.7'
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                           house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:569994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ274419
```

source

FEATURES

BASE COUNT

ORIGIN

DEFINITION

AQ274419

RESULT

셤 ò

ACCESSION VERSION KEYWORDS ORGANISM

ö

Gaps

```
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 AATGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AACGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numan.
                                                                                                                                                                                                                                                         40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
AQ212765
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 49.2)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
702 (206) 616-3887
Fax: (200) 616-3887
Fax: (200-604) Clones and be purchased from 10 the form of the following the fo
library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ406794 492 bp DNA GSS 17-MAR-1999 HS_5103_B2_G10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=679 Col=20 Row=N, genomic survey sequence. AQ406794 GI:4429416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 CAAAAATTGAAAAACTAGATCTATTTATTGCACGGGCGGCCGCCATGGGCCCGGCCGCCAAC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="Fraxon:9606"
-dlone="Plate=679 Col=20 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                 188 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                           1. .1201
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosBAC"
/clone="BACN15C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.1%; Score 25.6; DB 83; Best Local Similarity 32.8%; Pred. No. 1.4e+02; Matches 20; Conservative 26; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                 275 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 492.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 679 row: N column: 20 Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.htsc.washington.edu
                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                 /note="end: SP6"
204 c 230 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                       pBeloBAC11
                                                                                                                                                                                                                                                                                                                                                                                                                       304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G 64
                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
AQ406794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          å
```

4)

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holzman, T.,
Adams, M.D. and
                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ב
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
pBACe3.6; Genomic sequence of BAC ends"
93 g 131 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                     239 GGACATATACTGGATATTGAGAACTCAATGGTGAACAAGGCTGACATGCGCCCTGCCTC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ212765 507 bp DNA (GSS 18-SEP-1998 HS_3115_B2_H11_MR CIT Approved Human Genomic Sperm Library D H saplens genomic clone Plate=3115 Col=22 Row=P, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 501)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, 7
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Journal on Sep 10, 1998 this sequence version replaced gi:3553850.

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3808
Fax: (206) 616-3808
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Sequence Tagged Connector
Plate: 3115 row: P column: 22
Class: BAC ends
                                                                                                                                                          Gaps
                                                                                                                                                                                                   1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGGCCCGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.2%; Score 25; DB 99; Length 507; Best Local Similarity 69.4%; Pred. No. 2.4e+02; Matches 34; Conservative 0; Mismatches 15; Indels
                                                                                                             Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GCCAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGG
                                                                                                                                                          25;
                                                                                                               Score 25; DB 106;
Pred. No. 2.4e+02;
                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: :
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 g
  /note="Vector:
96 c 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQŽ12765
AQZ12765.1 GI:3623966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           в-со11 риї0в'
                                                                                                             36.2%;
milarity 61.5%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 c
                                                                                                               Query Match
Best Local Similarity
```

ORGANISM

KEYWORDS SOURCE

ACCESSION

RESULT AQ699107

REFERENCE AUTHORS

JOURNAL MEDLINE COMMENT

TITLE

```
Eukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

RS 2 hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.

Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building

Unpublished (1997)

Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850

Fax: 301 838 0200

Fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ384188 658 bp DNA GSS 21-MAY-1999
RPCII1-122P9.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-122P9,
genomic survey sequence.
AQ384188
AQ384188.1 GI:4355211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 658)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
1 116 c 120 g 148 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.2%; Score 25; DB 106; Length 603;
llarity 61.5%; Pred. No. 2.4e+02;
Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB.7567938"
/db_xref="taxon:9606"
/clone="RRCI-11-177019"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1997)
Other_GSSs: RPCII1-122P9.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATGG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AACGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
ORGANISM
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297
                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                 REFERENCE
                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ384188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On Sep 10, 1998 this sequence version replaced gi:3555646.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3817
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, plasse contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPRC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1136 row: J column: 2
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 516)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 103~{
m c} 107~{
m g} 127~{
m t} 6 others
                                                                                          AQ699107 516 bp DNA GSS 06-JUL-1999 HS_5560_B2_E01_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=2 Row=J, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 GGACATATACTGGATATTGAGAACTCGATGGTGAACAAGGCTGACATGCGCCCTGCCTC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ415486 603 bp DNA GSS 23-
RPCT-11-177019. TJ RPCT-11 Homo sapiens genomic clone
RPCT-11-177019, genomic survey sequence.
AQ415486.1 GI:4474455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 516.

Location/Qualifiers

1. 516
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1136 Col=2 Row=J"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 85; Length 516;
Pred. No. 2.4e+02;
0; Mismatches 25; Indels
                                                                                                                                                                                        AQ699107
AQ699107.1 GI:5389355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.2%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40; Conservative
                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 AACGG 65
                                                                                             LOCUS
DEFINITION
```

BASE COUNT ORIGIN

FEATURES

Matches

g ò ద DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

RESULT 8 AQ415486 LOCUS

296

ö

Gaps

```
mRNA sequence.
                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                     Query Match
Best Local S:
Matches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW276836/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                              Documents.

Location/Qualifiers

1. 658

/Organism="Homo sapiens"
/db_xref="cbb:7546832"
/db_xref="cbb:7546832"
/db_xref="cbb:7546832"
/db_xref="cbb:71112229"
/close_lib="RPCI-111"
/sex="Male"
/cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"

RPCIII Human Male BAC Library"

15 a 128 c 126 g 169 t
                                                                                 Email: hbeetigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: SP6

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW265066 426 bp mRNA EST 28-DEC-1999 xq60q03.x1 NCI_CGAP_CC22 Homo sapiens cDNA clone IMAGE:2755060 3/ similar to SW:E411_ADE02 P03241 PROBABLE EARLY E4 11 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 426)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAtional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Jul 7, 1999 this sequence version replaced gi:5406301.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCGGCCATGGGCCCGGCCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown library type
Possible reversed clone: similarity on wrong strand
Possible reversed clone: polyT not found
Seq primer: -40UP from Glbco
High quality sequence stop: 425.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
The Institute for Genomic Research 9712 medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 106;
Pred. No. 2.4e+02;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2755060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]; mRNA sequence.
AW265066
AW265066.1 GI:6641882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 36.2%;
1 Similarity 61.5%;
40; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 40; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 AATGG 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 AACGG 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
AW265066/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
```

```
Homo saplens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 630)

NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-GCAP http://www.ncbi.nlm.nih.gov/ncicgap.

Numor Gene Index

Unpublished (1997)

On Nov 22, 1999 this sequence version replaced gi:6462296.

Contact: Robert Straubberg, Ph.D.

Tel: (301) 496-1550

Email: Robert-Straubberg, Ph.D.

Tel: (301) 496-1550

Email: Robert-Straubberg, Ph.D.

Tolsue Procurement: Andrew Berchuck M.D., John Gillespie M.D.,

Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CONG distribution: NCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: ovary; Vector: pAMP10; cDNA made by oligo-dr
priming. Non-directionally cloned into the UDG sites of
pAMP10. Size-selected on agazose gel, average insert
size 500 bp. Primary library; non-amplified. cDNA
Library Preparation: David B. Krizman, Ph.D (NCI).
Reference: Krizman et al. (1996) Cancer Research
                                                                                             /note="Organ: colon; Vector: pAMPIO; cDNA made by oligo-dT priming. Non-directionally cloned into the UDG sites of pamping. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D (NCI). Reference: Krizman et al. (1996) Cancer Research 55380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW276836 630 bp mRNA EST 03-JAN-2000 xp66911.x1 NCI_CGAP_Ov39 Homo sapiens cDNA clone IMAGE:2745380 3' similar to SW:E413_ADE02 P03240 PROBABLE EARLY E4 13 KD PROTEIN. ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="papillary serous ovarian metastasis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Possible reversed clone: similarity on wrong strand Possible reversed clone: polyT not found Seq primer: -40UP from Gibco High quality sequence stop: 422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
/clone_lib="NCI_CGAP_CO22"
/tissue_type="colonic adenocarcinoma"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.9%; Score 24.8; DB 79;
Local Similarity 63.3%; Pred. No. 2.8e+02;
Nes 38; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:2745380"
/clone_lib="NCI_CGAP_0v39"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .630
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW276836.1 GI:6663866
```

ద

ö

Ĵ

```
1. .194
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9823"
/clone_llb="MARC 2PIG"
                                                                                                                                                                                                                                                                                                       FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTATCCAGACACGACG
Plate: 13 row: A column: 24
Seg primer: ATTAGGTGACACTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ064961
AQ064961.1 GI:3380789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ064961/c
                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
COMMENT
                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                    Oryctolagus cuniculus.
Oryctolagus cuniculus
Oryctolagus cuniculus
Bukaryota: Metacoa: Chordata; Craniata; Vertebrata; Mammalla;
Butaryota: Lagomorpha; Leporidae; Oryctolagus.
1 (bases 1 to 379)
Nobori,M., Ikeda,Y., Nara,H., Kato,M., Kumegawa,M., Nojima,H. and
                                                                                                                                                                                                                                                                                                                                                                                                          Large scale isolation of osteoclast-specific genes by an improved method involving the preparation of a subtracted cDNA library genes Cells 3 (7), 459-475 (1998)
                                                                                                                                                                                                                                C84505 379 bp mRNA EST 26-MAR-1999 C84505 osteoclast subtracted library Oryctolagus cuniculus cDNA, mRNA sequence.
                                                                                                                              Contact: Kobori M
Molecular Medicine Laboratories
Institute for Drug Discovery Research, Yamanouchi Pharmaceutica
21, Miyukigaoka, Tsukuba, Ibaraki 305, Japan
Emali: kobori@yamanouchi.co.jp
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jun 5, 1998 this sequence version replaced gi:3189094
                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 48; Length 379;
                                                                       Length 630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryctolagus cuniculus"
/db_xref="taxon:9986"
/clone_lib="osteoclast subtracted library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW354184 194 bp mRNA EST (
32589 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW354184.1 GI:6853174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        others
                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
               _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16
                                                                    Query Match 35.9%; Score 24.8; DB 79; Best Local Similarity 63.3%; Pred. No. 2.7e+02; Matches 38; Conservative 0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 24.6; DB 48;
Pred. No. 3.3e+02;
0; Mismatches 25;
               ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ų
             168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="long bone"
/cell_type="osteoclast"
/cell_line="primary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="5 day-old"
125 c 108 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                ρ
            173
56:5380-5383."
a 134 c 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sh 35.7%;
L Similarity 60.9%;
39; Conservative (
                                                                                                                                                                                                                                                                                        C84505.1 GI:4527765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .379
             154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGG 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S:
Matches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
ACCESSION
VERSION
KEYWORDS
            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                      12
                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW354184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
```

셤

õ

g

ò

```
Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutharyota; Cetaricodactyla; Suina; Suidae; Sus.

Eutharyota; Cetaricodactyla; Suina; Suidae; Sus.

1 (bases 1 to 194)

RS Fahrenkrugh,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A. and Keele,J.W. Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

ND Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine

On May 18, 1998 this sequence version replaced gi:3138121.

Contact: Smith TPL

Fax: 402 762 4390

Email: smith@email.marc.usda.gov

Single pass sequencing. Bases called and trimmed with phred

vo.980904.e. Vector identified by cross_match with the -minscore 20

and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holzman,T.,
Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pGMV SPORT6; Site_1: Xba1; Site_2: Xho1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 50 c 93 g 18 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ064961 355 bp DNA GSS 04-AUG-1998 HS_2225_A1_G06_MF CIT Approved Human Genomic Sperm Library D F sapiens genomic clone Plate-2225 Col-11 Row-M, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.

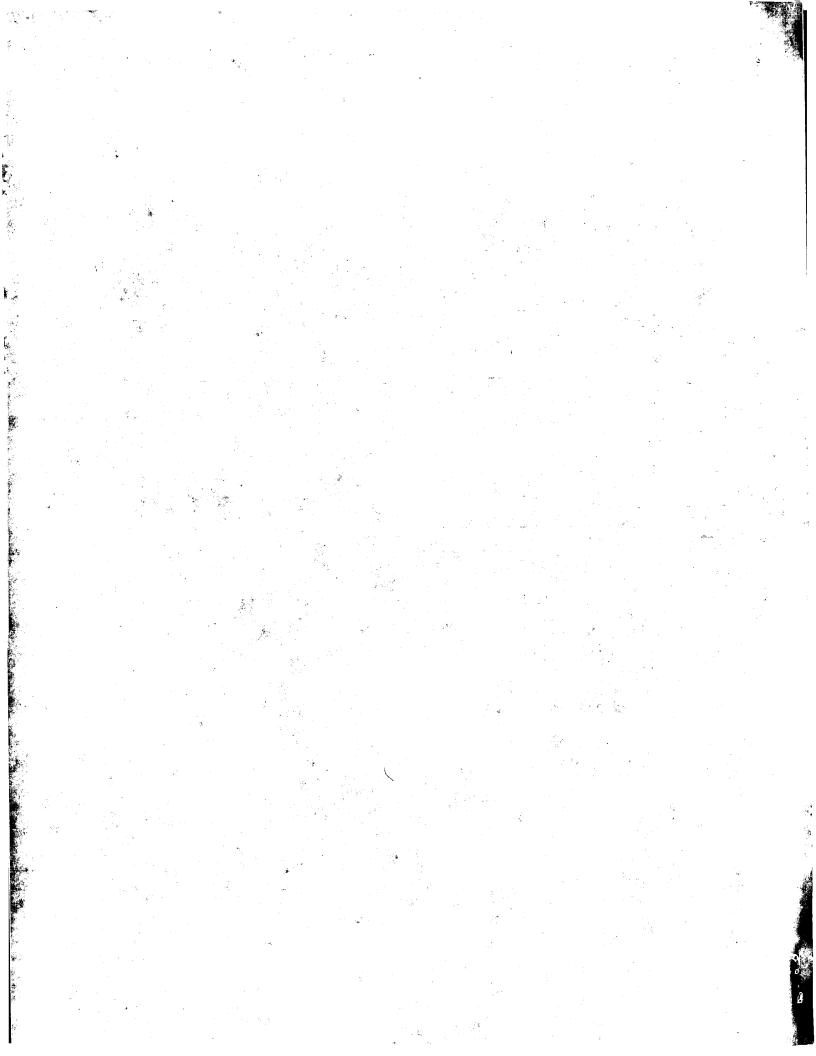
[ (base: 1 to 355)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, Keller, A., 'Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 TGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGGCCCGGCCGCCAACGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.4%; Score 24.4; DB 80; Length 194; llarity 63.8%; Pred. No. 4.1e+02; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Doi, H. Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst Systematic analyses of genes expressed in 3.5-dpc mouse blastocyst (The ERATO/Doi Project at Wayne State University) Unpublished (1997) on May 5, 1995 this sequence version replaced gi:797882. Contact: Hirofuni Doi Doi Bloasymmetry Project, ERATO Japan Science and Technology Corporation (JST) WBG Marive East 12F, 2-6 Nakase, Mihama-Ku, Chiba 261-71, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 578)
Ko, M.S.H., Kitchen, J.R., Wang, X., Wang, X., Threat, T.A., Sun, T.,
Grahovac, M.J., Mason, S., Lim, M.K., Paonessa, P.D., Sauls, A.D. and
                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="plate=2225 Col=11 Row=M"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
F-Coli DH10B"
71 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C78547 578 bp mRNA EST 25-JUN-1998 C78547 Mouse 3.5-dpc blastocyst cDNA Mus musculus cDNA clone J0051B03 3' similar to Mus musculus transcription factor like protein 4 TCFL4, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CAAAAAITGAAAAACTAGAICTAITIAITGCACGCGGCCGCCAIGGGCCCGGCCGGCCAA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 35.4%; Score 24.4; DB 36; Length 578; Best Local Similarity 62.7%; Pred. No. 3.7e+02; Matches 37; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .578
/organism="Mus musculus"
/stran="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0051B03"
/clone_1lib="Mouse 3.5-dpc blastocyst cDNA"
/tissue_type="blastocyst"
/dev_stage="3.5-dpc"
/dev_stage="3.5-dpc"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 24.4; DB 96; Length 355;
Pred. No. 3.9e+02;
0; Mismatches 11; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGC 44
Tel: (206) 616-3618
Fax: (206) 616-3887
Fax: (206) 616-3887
Faylace@u washington.edu
Spaquence Tagged Connector
Plate: 2225 row: M column: 11
Class: BAC ends
High quality sequence stop: 355.
High quality sequence stop: 355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hd@bioa.jst.go.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.4%;
Best Local Similarity 73.8%;
Matches 31; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278547
278547.1 GI:2518877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
C78547/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

ŏ

```
셤
```

Search completed: May 29, 2000, 21:13:10 Job time: 36509 sec



Run on:

```
ņ
                                                                                                                                                                                                             æ
                                                         May 29, 2000, 21:33:53; Search time 1214.87 Seconds (without alignments) 470.244 Million cell updates/sec
                                                                                               US-08-935-377-3
75
1 GGCCAAAAATTGAAATTTTA......GCCCGGCCGCCAACGGCGGA 75
                                                                                                                                                                                         1765538
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                     882769 segs, 3808571567 residues
                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM nucleic - nucleic search, using sw model
                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                          gb_sy:*
gb_un:*
gb_v1:*
em_fun:*
em_hum1:*
em_hum2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_htg1:*
gb_htg2:*
                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                          90 bal: *
90 bli: *
90 bli: *
90 bli: *
90 bri: *
90 bri: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_pr4:*
gb_htg3:*
gb_htg4:*
gb_htg5:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_in1:*
gb_in2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_hum3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_hum4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_pat:*
em_ph:*
em_pl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_ro:*
em_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_om: *
em_or: *
em_ov: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             еm_sy:*
еm_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_v1:*
                                                                                                                                                                                                                                                                                   GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                    Searched:
                                                                                                                      Seguence:
```

```
9b_htg6:*
em_htg1:*
em_htg2:*
em_htg3:*
em_htg3:*
em_htg3:*
em_htg3:*
gb_htg8:*
gb_htg9:*
gb_htg9:*
gb_htg1:*
gb_htg1:*
gb_htg1:*
gb_htg1:*
gb_htg1:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ഗ
ω
н
ĸ
₹
ξ
Σ
5
้

sult		% Query			1	
	Score	Match	Length	8	. ai	Description
	Θ.		21		VH3FDPC	356 V.virus
	40.6	54.1	2164	19	[14	9857 V.virus D
	40	m	84	വ	m	59039 Sequence
	4	'n		Ŋ	59040	10 Seguence
	32.4		160821	54	124	12468 Homo sa
	ᆏ	ä	310		3924	Homo sa
	31	ä	43		1113	Mouse int
	31	ä	595		574	12 Mus mus
	m	;	63		88	886 Mus
	ö		017		83	895
	ö		614		AC005341	11 Homo
	ö		619		67	672 Homo
	ę.		080		56	26 Arabid
	6.		416		361	751 Homo
	φ.		183		101	15 Homo
	ė.		183		HSJ324017	L5 Homo
	ď.		29		W5	Homo sa
	e.	ď	832		AC009833	33 Homo
	ď	σ.	56		32	18 Mus π
	6	6	351		52	24 Drosoph
	29.4		S		$\sim$	AF101319 Caenorhab
	σ.	ω.	59		5F	Caen
	٩.	8	340		391	Ω 2
	e,	œ.	22		344	
	φ.	œ	791		264	11 H
	œ.	œ	270		587	7 0
	6.	ω.	988		591	11 CE
	29	8	15		3	Caer
	29	ω.	34		356	3 Drosophi
	29		8		9	ation (6
	29	æ	41		532	328 Homc
	29		12		846	162 Homo s
	œ.		14		HS15D7	229 Human
	œ.		63	40	046	165 Homo
	ω.		492	43	366	568 Homo
	ω,		15	54	580	5809 Homo
	ω.		650	41	551	5517 Homo
	ω.		561	41	_	3139 Plasm
	ω.		74	35	032	327 P.
	ω.		78	34	K48	2298
	8		9	6	_	1077 HOT
	28.6	38.1	38561	41	990	06604 Caenorha
	ъ.		36	11	1420	14209 Homo sa
	8		0	σ	AP000514	Homo sa
	œ.		015	41	290	06793 Caenorh

ALIGNMENTS

615

ρ 475

O

488

586

```
/product="hygromycin phosphotransferase"
/product="hygromycin phosphotransferase"
/product="caa61953.1"
/db_xref="G1:953211"
/db_xref="G1:953211"
/tb_xref="SWISS-PROT"
/translation="WKKPEIJATSVPKFLIEKFDSVSDLMQLSEGEESRAFSFDVGGR
/translation="WKKPEIJATSVPKFLIEKFDSVSDLMQLSEGEESRAFSFDVGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="NOT cleavage site corresponding to the unique NOT I site in the VV genome at position 45478 (strain copenhagen)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter.
Vaccinia virus.
Vaccinia virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 AAAAATTGAAATTTTATTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCGGCCG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Direct Submission
Submitted (20-JUL-1995) M. Pfleiderer, Immuno AG, A. 2304
Submitted (20-JUL-1995) M. Pfleiderer, Immuno AG, A. 2304
OrthDonau, Uferstrasse 15, AUSTRIA
Related sequence M35027.

Related sequence M35027.

1. 2164 / Organism="Vaccinia virus"
/ Strain="WR"
/ Strain="WR"
/ Specific host="mammalians"
/ db_xref="taxon:10245"
/ lb_host="mammalian cell lines"
/ cell_line="recombinant Vaccinia virus"
/ clone="WDPC 2"
                                                                                                                                                                                                                                                                                                                                                                                                          X88857.1 GI:927569
Hindili F fragment; hph gene; hygromycin phosphotransferase;
                                                                                                     ö
                                                                 Length 2164;
                                                                                                                                                                                                                                                                                                                                       VVH3FDPC2 2164 bp DNA Vrirus DNA for Hind III F fragment (clone VDPC2). X89857
                                                                 Score 40.6; DB 16;
Pred. No. 0.038;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Rsr II cleavage site"
complement(506. .1531)
/gene="hph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(479. .1642)
/note="NOT I gene cassette"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(506. .1531)
/gene="hph"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="45478 nt number"
                                                                   54.1%; 73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 2164)
Pfleiderer, M.
                                                                 Query Match
Best Local Similarity 73.28
Matches 52; Conservative
                                                                                                                                                                                                                                                             548 TAAAAGTTGAA 558
                                                                                                                                                                                                                       65 CCAACGGCGGA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96112180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                       RESULT 2
VVH3FDPC2/c
                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                               g
                                                                                                                                                                                     g
                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPETELPAVLOPVAEAMDAIAAADLSOTSGFGFFGFGGGGGGYTWRDFICAIADFWY
HWQTVMDDTWSASVAQALDELMLWAEDCPEVRHLVHADFGSNNVLTDNGRITAVIDHS
EAMFGDSQYEVANIFFWRPWLACMEQQTRYFERRHPELAGSPRLRAYMLRIGLDOLYO
SLVDGNFDDAAWAQGRCDAIVRSGAGTVGRTQIARRSAAVWTDGCVEVLADSGNRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation-"MKKPELIATSVEKFLIEKFDSVSDLMQLSEGEESRAFSFDVGGR
GYVLRVNSCADGFYKDRXVYRHFASAALPIPEVLDIGEFSESLTYCISRRAQGVTLQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="NOT I cleavage site corresponding to the unique NOT I site in the Vv genome at position 45478 (strain copenhagen)"
                                                                                                                                                                                     Vaccinia virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Orthopoxvirus.
                                                                                                                                                                                                                                                                         (bases 1 to 2164)
Pleiderer,M., Falkner,F.G. and Dorner,F. A novel vaccinia virus expression system allowing construction of recombinants without the need for selection markers, plasmids and
                                                                             03-JAN-1996
                                                                             VVH3FDPC1 2164 bp DNA VRL 03-JAN-199 V. virus DNA for Hind III F fragment (clone VDPC1). 3-JAN-199 V. virus DNA for Hind III F fragment (clone vDPC1). 3-JAN-199 V. virus DNA for HindIII F fragment; hph gene; hygromycin phosphotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-70L-1995) M. Pfleiderer, Immuno AG, A. 2304
Orth/Donau, Uferstrasse 15, AUSTRIA
Related sequence M35027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486. .543
/note="strong synthetic early/late promoter"
536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544. .594
/note="weak synthetic early/late promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product-"hygromycin phosphotransferase"
Perotein_id="CAA61952.1"
/db_xref="G1:9531.0"
/db_xref="G1:9531.0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /specific_host="mammalians"
/db_xref="taxon:10246"
/db_host="mammalian cell lines"
/cell_line="recombinant Vaccinia virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note-"unique Sfi I cleavage site'
                                                                                                                                                                                                                                                                                                                                                     Dacterial hosts
J. Gen. Virol. 76 (Pt 12), 2957-2962 (1995)
96112180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Rsr II cleavage site"
1642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="NOT I cleavage site"
1643. .2164
/note="Hind III F fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179. .1662
/note="NOT I gene cassette"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Hind III F fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 2164
/organism="Vaccinia virus"
/strain="WR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="45478 nt number"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="VDPC 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           595. .1620
/gene="hph"
595. .1620
/gene="hph"
                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 2164)
Pfleiderer,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPRAKE"
                                                                                                                                                                                   promoter.
Vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                     LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                 RESULT 1
VVH3FDPC1
```

COMMENT

SOURCE

ö

28

o o

```
1 (bases 1 to 86)
Schefflinger, F.D., Antoine, G.D., Falkner, Falko-Guenter, D.,
Dorner, F.P. and Eibl, J.D.
Improved recombinant eukaryotic cytoplasmic viruses, method for
their production and their use as vaccines
Patent: EP 0753581-A 28 15-JAN-1997;
IMMUNO AG (AI)
                                                                                                                                                                                                                                                                                                                                        Ouery Match 53.3%; Score 40; DB 5; Length 86; Best Local Similarity 82.1%; Pred. No. 0.038; Matches 46; Conservative 0; Mismatches 10; Indels

    .86
    /organism="unidentified"
    /db_xref="taxon:32644"

                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                   11 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Data
Unpublished
unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases
Smith, D.R.
                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                ORGANISM
                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                    AC012468
                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                       g
              HWOTVMDDTVSASVAQALDELMLWAEDCPEVRHLVHADFGSNNVLTDNGRITAVIDWS
EAMFGDSQYEVANIFFWRPWLACMEQQTRYFERRHPELAGSPRLRAYMLRIGLDQLYQ
SLVDGNFDDAAWAQGRCDAIVRSGAGTVGRTQIARRSAAVWTDGCVEVLADSGNRRPS
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 84)
Schellinger,F.D., Antoine,G.D., Falkner, Falko-Guenter,D.,
Schellinger,F.D. and Eibly.D.
Dorner,F.P. and Eibly.D.
Improved recombinant eukaryotic cytoplasmic viruses, method for
their production and their use as vaccines
Patent: EP 0753581-A 27 15-JAN-1997;
IMMDNO AG (AT)
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                        5 AAAAATTGAAATTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCGGCCG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CCAAAAATTGAAATTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                            Length 2164;
                                                                                                       /note="Sfi cleavage site"
complement(1598. 1639)
/note="strong synthetic early/late promoter"
1642
                                                               complement(1532. .1585)
/note="weak synthetic early/late promoter"
1592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 5; Length 84;
Pred. No. 0.038;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                                                                                                                                                                                                                                                                            54.1%; Score 40.6; DB 16;
illarity 73.2%; Pred. No. 0.038;
Conservative 0; Mismatches 19;
                                                                                                                                                                                                1643. .2164
/note="Hind III F fragment"
524 c 439 g 606 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 t
                                                                                                                                                                                   /note="NOT I cleavage site"
1643. .2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .84
/organism="unidentified"
/db_xref="taxon:32644"
a 8 c 10 g 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A59039 84 bp DNA
Sequence 27 from Patent EP0753381.
A59039.1 GI:3714474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A59040 86 bp DNA
Sequence 28 from Patent EP0753581.
A59040.1 GI:3714475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 53.3%;
Best Local Similarity 82.1%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1578 TAAAAGTTGAA 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                      65 CCAACGGCGGA 75
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28
                                                                                                                                                                                                                                  595
                                                                                                          misc_feature
                                                                                                                                                                                                   misc_feature
                                                                             promoter
                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
A59040/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          င်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Direct Submission
Submitted (28-OCT-1999) Genome Therapeutics Corporation, 100 Beaver
Street, Waltham, MA 02453, USA
On Jan 14, 2000 this sequence version replaced gi:6682197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insert size: 160821; sum-of-contigs
Quality coverage: 4.1x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                  Genome Therapeutics Corporation Sequencing Center: Human Genome
AC012468 160821 bp DNA HTG 03-FEB-2000 Homo sapiens clone RP11-179H18, WORKING DRAFT SEQUENCE, 29 unordered pieces.
                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 160821)
Smith,D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                           AC012468
AC012468.5 GI:6693085
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 160821)
```

```
Enkaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Enkaryota; Metazoa; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Estanson, M., Agams, C., Aenson, A., Bailey, M., Barbaria, J.,

Blankenburg, K., Dedota, B., Bouck, J., Carter, M., Chacko, J., Chan, Z.,

Bunac, C., Burkett, C., Burrows, J., Carter, M., Chacko, J., Chan, Z.,

Bunac, C., David, K., Delgado, O., Deshazo, D., Ding, Y., Domen-Rashid, N.,

Eovarm-Tansey, J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Fernatz, P., Ganesh, R., Gorrell, J. H., Gorrell, J. L.,

Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,

Holloway, C., Hosak, H., Jackson, L., Jackson, L., Jackson, L.,

Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,

Lichtarge, O., Liu, J., Liu, W., Liogan, O., Lud, J., Lutler, R.,

Lichtarge, O., Liu, J., Liu, W., Logan, O., Lud, J., Lutler, R.,

Martin, R., Martinez, C., McLeod, M. P., Mei, G., Morgan, M., Martin, S.,

Raiten, D., Rives, M., Samuel, S., Sap, J., Scherer, S., Shah, E.,

Shen, H., Simon, M., Sparks, A., Stamps, A., Stamps, A., Stamps, A., Stamps, A., Weinstock, G., Weinstock, I. R., Williamson, A., Worley, K., Wren, J.,

Wrensford, G., Yu, W., Zhou, X. and Gibbs, R.,

Direct Submission

'L. Dupublished

L. Dupublished

L. Dupublished

L. Dupublished

L. Dupublished

L. Dupublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OB-AUG-1999) Human Genome Sequencing Center, Department Submitted (OB-AUG-1999) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA ON Sep 2, 1999 this sequence version replaced gi:5787982.

* NOTE: This is a "vorking draft, sequence. It currently consists of 96 contigs. The true order of the pleces arbitrary. Gaps between the contigs are represented as * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
                                                                                                  AC009246 331068 bp DNA HTG 03-SEP-1999
Homo sapiens, *** SEQUENCING IN PROGRESS ***, 96 unordered pieces.
AC009246
 unknown length
g of 16958 bp in length
id unknown length
of 15033 bp in length
of 18033 bp in length
of unknown length
ig of 10745 bp in length
of unknown length
of 10745 bp in length
of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74449; contig of 74449 bp in length
74469; gap of unknown length
91427; contig of 16958 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 8130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 6260
unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unki
contig of
gap of unki
contig of
gap of unki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 331068)
Worley, K.C.
                                                                                                                                                           AC009246.7 GI:5819117
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170629:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved.
                                                                                                                                                                                                       human.
                                                                                        RESULT 6
AC009246/c
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 54; Length 160821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 14860 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 16559 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 10040 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
                                                                                                                                                                                                                                                                                                                        ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                        ength.
                                                                                                                                                                ength
                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           닦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone_lib="RPCI-11"
36669 c 36666 g 44015 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
43.2%; Score 32.4; D
Best Local Similarity 71.2%; Pred. No. 15;
Matches 42; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 3730 l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
of 5890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-179H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                  contig e
gap of e
gap of e
contig e
gap of e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap ot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76568: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86608: contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101468: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                gap of
contig
gap of
                                                                                                                                                                                                                                                                             contig
qap of
                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66645: contig
                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
                                                                                                                                                                                                               contig
                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                               contig
                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118027:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140795:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160821:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44764:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50654:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58608:
                                                                                                                                                                                                                                                                                                                                                                     15433:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22735:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27919:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31649:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37383:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41600:
                                                     1162:
                                                                                   2431:
                                                                                                                   3867:
                                                                                                                                                                               6952:
                                                                                                                                                                                                               8125:
                                                                                                                                                                                                                                               9518:
                                                                                                                                                                                                                                                                                                                                                                                                       17627:
                                                                                                                                                                                                                                                                                                                                                                                                                                   19656:
                                                                                                                                                 5091:
                                                                                                                                                                                                                                                                             10648:
                                                                                                                                                                                                                                                                                                           11759:
                                                                                                                                                                                                                                                                                                                                           13202:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41601
                                                                                     1163
                                                                                                                     2432
                                                                                                                                                   3868
                                                                                                                                                                                 5092
                                                                                                                                                                                                                                               8126
                                                                                                                                                                                                                                                                               9519
                                                                                                                                                                                                                                                                                                           10649
                                                                                                                                                                                                                                                                                                                                           11760
                                                                                                                                                                                                                                                                                                                                                                           13203
                                                                                                                                                                                                                                                                                                                                                                                                       15434
                                                                                                                                                                                                                                                                                                                                                                                                                                     17628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25120
                                                                                                                                                                                                               6953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
length
bp in length
                                                               Jp ...
length
'n length
                                                                                 length
bp in length
                                                                                               length
bp in length
length
bp in length
                                                                                                                                                                                              length
bp in length
                                                                                                                                                                                                                                        length
bp in length
length
bp in length
                                                                                                                                                                                                                                                                  length
bp in length
                                                                                                                                                                                                                                                                                                                                                              Jp 1..
length
'n length
                                                                                                                                                                                                                                                                                                                                                                               length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                             length
bp in length
  length
bp in length
length
                           length
bp in length
                                                                                                                          length
bp in length
                                                                                                                                        length
bp in length
                                                                                                                                                                                                            length
bp in length
                                                                                                                                                                                                                                                                                length
bp in length
                                                                                                                                                                                                                                                                                             length
bp in length
                                                                                                                                                                                                                                                                                                           length
bp in length
                                                                                                                                                                                                                                                                                                                         length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                         length
bp in length
                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                                                                                       length
bp in length
                                          length
op in length
                                                                                                                                                        length
op in length
                                                                                                                                                                     lèngth
bp in length
                                                                                                                                                                                   length
bp in length
                                                                                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                                                                                            length
op in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in length
                     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                             in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in length
                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                             of 2049
                                                                                   unknown
                                                                                                                                          unknown
                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                 of 4417
                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                 ĕ
                                                                                                                                                                                                                                                                                         ğ
                                                                                                                                                                                                                                                                                                                                                                                          ö
contig
                                                                    gap of contig gap of contig
                                                                                                              gap of
contig
gap of
contig
                                                                                                                                          gap of
contig
                                                                                                                                                       gap of
contig
gap of
                                                                                                                                                                           contig
                                                                                                                                                                                   gap of
contig
gap of
contig
                                                                                                                                                                                                             gap of contig gap of contig
                                                                                                                                                                                                                                         gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                   gap of contig gap of gap of contig contig gap of contig gap of contig gap of contig gap of contig gap of
                                                                                                                                                                                                                                                                                                                                                      gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                  gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                            gap of contig gap of contig gap of contig
                                                                                                gap of
contig
                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279784:
279804:
281282:
                                                         96895:
                                                                                                              13218
13238
117098
217118
220902
224583
224603
                                                                                                                                                                                                                                                                  8485
8505
                                                192459
196896
201162
201182
201182
205311
205337
209337
                                                                                                                                                                                                                                                     5760
                                                                                                                                                                                                                                                                                                             475
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279805
```

Gaps Score 31.8; DB 41; Length 331068; Pred. No. 25; 0; Mismatches 17; Indels 0; of 1082 bp in length funknown length of 1073 bp in length funknown length of 1067 bp in length funknown length of 1065 bp in length op in length length bp in length length op in length ength in length length length length length in length op in length length in length length length bp in length length length length of 993 bp in length unknown length of 985 bp in length 956 bp in length known length 923 bp in length length length 919 bp in length length of 876 bp in length of yr.
unknown lens
of 904 bp in lens
m length 981 bp in ler known length op in 1 Length length p in 1 ength ength ength. length ength length ength length unknown length length unknown length <del>1</del>2 무 <del>1</del>2 r, unknown length unknown length of 889 bp in 890 bp in of 1229 R unknown of 1218 R unknown of 1214 R of 1214 R unknown of 1278 unknown of 1275 unknown of 1230 unknown of 1141 unknown of 1135 unknown of 1316 1245 1242 1265 unknown unknown unknown unknown 1366 unknown unknown unknown unknown of of of ŏ ŏ ō ō ö ŏ gap of contig gap of contig gap of contig contig gap of contig gap of contig gap of contig contig gap of contig contig gap of contig gap of contig gap of contig gap of contig contig gap of contig contig contig contig gap of gap of gap of gap of 42.48; 71.28; 316578: Query Match
Best Local Similarity 71.2
Matches, 42, Conservative 285442 285442 286778 286798 288076 388096 315683 7093 078 08078 82728 84094 290656 290676 291921 g δ

ö

RESULT

```
Kadner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C. H.

Direct Submission
Submitted (01-0CT-1998) Human Genome Center, DOE Joint Genome Institute, Lawrence Berkeley National Laboratory, MS 74-157, Berkeley, CA 94720, U.S.A.
Sequence Submitted by:

DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="GRAIL 2 excellent exon, frame 1"
23921. .23956
/note="(GT)18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frame 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       frame 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        290. .5410
note="GRAIL 2 excellent exon,
                                                                                                                               Location/Qualifiers
1. 159500
//Organism="Mus musculus"
//db_xref="taxon:10090"
//map="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_unit=AC
complement(21330. .21506)
                                                                                                                                                                                                                           /chromosome="11"
/note="LBNL M01"
complement(616. .691)
/rpt_family="Alu"
2368. .2409
/note="(CT)21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31377. .31420
./note="(CT)22"
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              t_type-tandem
                                                                                                                                                                                                                                                                                                                                                                                      rpt_type=tandem
rpt_unit=GT
                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_type=tandem
'rpt_unit=AC
                                                                                                                                                                                                                                                                                                                          'rpt_type=tandem
                                                                                                                                                                                                               /clone="111-181"
                                                                                                                                                                                                                                                                                                                                     /rpt_unit=CT
2522. .2559
/note="(GT)19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_unit=GT
26847. .26868
/note="(T)22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_unit=CT
31442. .31475
/note="(AG)17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_unit=AG
31706. .31743
/note="(AC)19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19242. .19279
/note="(AC)19"
                                                                                                                                                                                                                                                                                                                                                                                                                  3628. .3659
/note="(AC)16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pt_unit=ATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t_unit=AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pt_unit-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                           source
                                               TITLE
JOURNAL
                                                                                                                                         FEATURES
                                                                                                          COMMENT
                                                                                                                                                 Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4376)
McKenzia,A.N.J., Li,X., Largaespada,D.A., Sato,A., Kaneda,A.,
Zurawski,S.M., Doyle,E.L., Milatovich,A., Francke,U.,
Copeland,N.G., Jenkins,N.A. and Zurawski,G.
Structural comparison and chromosomal localization of the human and
mouse IL-13 genes
J. Immunol. 150, 8436-5444 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACO05742 159500 bp DNA ROD 01-OCT-1998
Mus musculus chromosome 11, BAC clone 111-181 (LBNL M01), complete
                                                                                     L13028.1 GI:309397
interleukin 13.
Mus musculus (strain BALB/c, sub_species domesticus) adult liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 159500)
Kimmerly, W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Radner, K., Miguel, T., Miller, C., Pitluck, S., Pollard, M., Sepseki, H., Subramanian, S. and Martin, C.H.
Sequencing of mouse chromosome 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
3 (bases 1 to 159500)
Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                  27-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 12; Length 4376;
Pred. No. 25;
                                    MUSIL13A 4376 bp DNA 2'
Mouse interleukin-13 gene sequence with four exons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 TIGAAAITITITITITITITITIGGAATATAAAGCGGCCGCCAIGGG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1046 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                /sub_species="domesticus"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 4376
/organism="Mus musculus"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="liver" <726. .934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=3
3240. .>4073
/number=4
a 1122 c 1146 g
                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/germline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC005742
AC005742.1 GI:3687208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 159500)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.3%;
Best Local Similarity 78.7%;
Matches 37; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jnpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಹ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricke, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
REFERENCE
AUTHORS
                                            LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                             MUSIL13A/c
                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
AC005742
                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                             TITLE
```

ò g

```
/rpt_type=tandem
/rpt_unit=TYGT
56295 .56481 2 excellent exon, frame 1"
56883 .57080
/note="GRAIL 2 excellent exon, frame 2"
57358 .57513
/note="GRAIL 2 excellent exon, frame 2"
59918 .59998
/note="GRAIL 2 excellent exon, frame 0"
61088 .61169
                                                                                                                                                                                                                                                                                      /rpt_family="Alu"

complement(39179. .39328)

/rpt_family="Alu"

4328. .43261

/rott="(GTTY)6"

/rpt_type=tandem

/rpt_unit=GTTT

43599. .43872

/note="GRAIL 2 excellent exon, frame 2"

44782. .44823

/note="(GT)21"
                                                                                                                                                                                                      36102...36260
/rpt_family='Alu"
36281...36381
/note="GRALL 2 excellent exon, frame 2"
complement(31129...37274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67345. .67485

// Anote="RAIL 2 excellent exon, frame 0"

67912. .68019

// Anote="GAIL 2 excellent exon, frame 0"

70200. .70225

// Anote="(GI)13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    frame 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_type=tandem
/rpt_tull=GT
5912. .52056
/note="GRAIL 2 excellent exon, fi
52168. .52252
/note="GRAIL 2 excellent exon, fi
52796. .52901
/note="GRAIL 2 excellent exon, fi
53966. .53993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="Alu"
63644. .63822
/note="GRAIL 2 excellent exon, f. 66362. .66598
/note="GRAIL 2 excellent exon, f. 66987. .67185
/note="GRAIL 2 excellent exon, f. 67087. .67185
                                                                          32283 .32431
/rpt_family="Alu"
3429. .34356
/rpt_family="Alu"
34339 .34359
/note="(A)21"
/rpt_type=tandem
/rpt_unit=A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_type=tandem
/rpt_unit=GT
47742. .47765
/note="(GT)12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_type-tandem
                                               /rpt_type=tandem
/rpt_unit=AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_unit=GT
45180. .45207
/note="(GT)14"
/rpt_unit=AC
31744. .31793
/note="(AG)25"
               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                               repeat_region
                                                                                                               repeat_region
                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                              repeat_region
                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
```

```
Direct Submission

Submitted (10-JAN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Dire, Walnut Creek, CA 94598, USA On Feb 16, 2000 this sequence version replaced gi:6686422.

* NOTE: This record contains 144 individual sequencing reads that have not been assembled into contains 144 individual sequencing reads that have not been assembled into and the order in which they appear is completely and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlat relationships among clones to be deduced.

* However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACO20886 196382 bp DNA HTG 16-FEB-2000
Mus musculus clone RP23-464K4, LOW-PASS SEQUENCE SAMPLING.
ACO20886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse.

Mus musculus

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 196382)

DOE Joint Genome Institute.

Sequencing of Mouse

Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 41.3%; Score 31; DB 12; Length 159500; Best Local Similarity 78.7%; Pred. No. 38; Matches 37; Conservative 0; Mismatches 10; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DD 107870 IIGAATITITITITITITITITIGGAAAATCCAGIGGCCGCTAAAGG 107916
                                                                        /note="GRAIL 2 excellent exon, frame 1" 79838, 79899 //note="(TC)31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_unit-GA
8607. 86052
/note="GRAIL 2 excellent exon, frame 0"
86454. 86489
/note="(CTIG)9"
                  /note-"GRAIL 2 excellent exon, frame 1"
71776. 71900
/note-"GRAIL 2 excellent exon, frame 0"
complement(73887. 73930)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 TICAAATTITATTITITITITITGGAATATAAAGCGGCCGCCAIGGG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_type=tandem
/rpt_unit=CTTG
complement(86625. .86682)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 196382)
DOE Joint Genome Institute.
                                                                                                                                                                                            /rpt_uiit=rc
80689. .80841
/rpt_family="Alu"
83589. .83612
/note="(AT)12"
                                                                                                                                                                                                                                                                                                                                               84528. .84579
/note="(AT)26"
/rpt_type=tandem
                                                                                                                                                                                                                                                                                                  /rpt_type=tandem
/rpt_unit=AT
                                                                                                                                                                       'rpt_type=tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'rpt_type-tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                   85024. .85065
/note="(GA)21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC020886.2 GI:6980213
HTG; HTGS_PHASE0.
                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_unit=AT
                                                                                                                                 repeat_region
                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
misc_feature
                                             misc_feature
                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
AC020886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

* 25699	* * 26801	* 27625	27849	* 28501	* 29387	* 30484	* 30733	* 32259	* 32966	* 33540	* 34631	* 35568	* 35665	* 36334	* 36717	* 37118	* 38277	* 39283	* 39654	* * 40168	* 40871	* * 41130	* 41400	* 41654 *	* 42291	* 43332 *	* 44500	* 45696 *	* 46508	* 47523	* 47758	* 48002	* 48612	* 49156	* 49256
																													-						
	_					-									- -			<u>.</u>												-					
ď	æ	ч.	æ	,c	<b>ب</b>	4	Æ,	ų.	th	ų	ų	lth	ન	ૡ	લ	f	લ	4.	yth	무	단	gth	сh	tЪ	th	gth	ţþ	랴	gth	gth	gth	th	gth	th	rth
bp in lengtl length	bp in lengtl	g of 278 bp in length length length	bp in lengt length	bp in lengt length	bp in lengt length	bp in lengt length	bp in lengt	bp in lengt	bp in leng	of 978 bp in length	bp in lengt	of 1020 bp in length unknown length	215 bp in length	623 bp in length	bp in lengt	bp in lengt	bp in lengt	bp in lengt	g of 1161 bp in length noknown length	bp in lengt	bp in lengt n length	6 bp in leng	bp in lengt n length	bp in leng. n length	of 721 bp in length unknown length	2 bp in len n length	bp in leng n length	bp in leng n length	8 bp in len	6 bp in len	12 bp in len	g of 935 bp in length f unknown length	'0 bp in len n length	of 787 bp in length	of 161 bp in length
of 855 lunknown	of 585	of 278	of 487 unknown	of 498 unknown	of 806	of 570 unknown	of 479	of 254	of 1111	of 978	of 614	of 1020	of 215 h	of 623	of 819	of 688	of 170	of 219	of 116.	of 786	of 426	of 104	of 109	of 856	of 721 unknow	y of 102	y of 108 mknow	y of 816 f unknow	of 101	g of 127	g of 120	g of 935 f unknow	g of 107	g of 787	
contig	contig	contig	contig qap of	contig qap of	contig	contig	contig	contig	contig	contig	contig	* PD#	contig	contig	contig	contig	3 4 6	3 - 7 7	contig	٠ <u>٠</u> , ٥	contig	contig	conti						contig	contig	contig	contig	contig	contic	cont
855:	1440:	1718:	2205:	2703:	3509:	4079:	4558:	4812:	5923:	6901:	7515:	8535:	8750:	9373:	10192:	10880:	11050:	11269:	12430:	13216:	13642:	14688:	14797:	15653:	16374:	17396:	17504:	18320:	19338:	20614:	21816:	22751:	23821:	24608:	24769:
	856	1441	1719	2206	2704	3510	4080	4559	4813	5924	6902	7516	8536	8751	9374	10193	10881	11051	11270	12431	13217	13643	14689	14798	15654	16375	17397	17505	18321	19339	20615	21817	22752	23822	24609

28800: contig of lutto be in length age of unknown length age of unknown length and age of unknown length as ontig of unknown length and age of unknown length age of

```
Dipublished

Stren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Blrren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Barra, N., Castle, A., Cerry, J., Cooke, P., Depayre, E., Boutwell, C., Brown, A., Castle, A., Cerry, J., Cooke, P., Depayre, E., EtzHqqi, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Fitzhqqi, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Garajery, K., Glumartin, T., Cann, L., Marchin, H., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Mardonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Malloff, M., O'Connor, T., Pavilin, B., Peterson, K., Riley, R., Roberts, D., Rossello, R., Roy, A., Shyam, R., Stone, C., Subramanian, A., Torruella-Miller, I., Vassiliev, H., Vo. A., Wagner, A., Wang, B., Wheeler, J., Wu, Y., Ye, W.J., Zhao, J. and Zody, M. Direct Submission

L. Submitted (30-JUL-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 161449)

Saliren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M. Baker, J., Baldwin, J., Barna, N., Beckelly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Coke, P., Deverlainon, Ferrettar, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC005341 161449 bp DNA PRI 29-JUL-1999
Homo sapiens chromosome 17, clone hRPK.146_P_2, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 161449)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.146_P_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Length 201746;
                                                    18247: gap of unknown length
23672: contig of 5430 bp in length
22625: gap of unknown length
22225: contig of 5533 bp in length
29240: gap of unknown length
37388: contig of 8148 bp in length
37403: gap of unknown length
69862: contig of 12459 bp in length
128770: contig of 32459 bp in length
128770: contig of 58893 bp in length
128785: gap of unknown length
128785: gap of unknown length
128785: contig of 72961 bp in length
                                                                                                                                                                                                                                                                                                                                                                                          165 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels

    .201746
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CCAAAAATTGAAATTTTTTTTTTTTTGGAATATAAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.4; DB
Pred. No. 59;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        37036 c 36424 g 64293 t
                      unknown
of 4019 1
                                                                                                                                                                                                                                                                                             location/Qualifiers
                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC005341
AC005341.12 GI:5649369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 40.5%;
il Similarity 85.0%;
34; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
10202
14199
114234
118233
118233
123678
23678
23622
23226
23226
37381
37404
69378
12878
                                                                                                                                                                                                                                                                                                                                                                                          63828 a
                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
AC005341/c
                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases I to 201746)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E 2 (bases 1 to 201746)

Waterston, R.H.

Direct Submission

Submitted (24-FEB-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Loui
MO 63108, USA

On Mar 1, 1999 this sequence version replaced gi:4263453.

* NOTE: This is a "working draft" sequence. It currently

* consists of 12 contigs. The true order of the pleces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* trus of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans clone Y71G12, *** SEQUENCING IN PROGRESS ***, 12 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 31; DB 55; Length 196382;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 194088 TIGAATTTTTTTTTTTTTTTTGGAAAATCCAGTGGCCGCTAAAGG 194134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :: contig of 2190 bp in length
:: gap of unknown length
:: contig of 2058 bp in length
:: gap of unknown length
:: contig of 2368 bp in length
:: gap of unknown length
:: contig of 3525 bp in length
:: gap of unknown length
                                                                                                                                                                                                               f unknown length
g of 856 bp in length
f unknown length
g of 1255 bp in length
g unknown length
g of 980 bp in length
f unknown length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Indels
                                                                                                                                                                                                                                                                                                                                                    of 1098 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
of 1120 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 ITGAAATTTTATTTTTTTTTGGAATATAAAGCGGCCGCCATGGG 56
                                        of 177 bp in length
unknown length
                                                                                                                                                        length
                                                                                                                                                                             unknown length
of 719 bp in length
                                                                                                                                                                                                                                                                                                                                                                                          577 bp in length
                                                                              of 407 bp in length
                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of Caehorhabditis elegans clone Unpublished
                      unknown length
                                                                                                  length
                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                                                                                                                    of 129 bp in
                                                                                                                                                          of 154 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                    unknown
                                                                                                                                      unknown
                                                          gap of contig gap of contig gap of contig gap of contig gap of contig
                                                                                                                                                                                                                 gap of contig
                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                    contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                gap of contig
                                        contig
                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                            contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC006895.2 GI:4309904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.3%;
78.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2190:
2205:
4263:
4278:
6646:
6661:
10186:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201746 bp
                                        51530:
                                                                              51937:
                                                                                                                52066:
                                                                                                                                                      52220:
                                                                                                                                                                                             52939:
                                                                                                                                                                                                                                 53795:
                                                                                                                                                                                                                                                                         55050:
                                                                                                                                                                                                                                                                                                             56030:
                                                                                                                                                                                                                                                                                                                                                    57128:
                                                                                                                                                                                                                                                                                                                                                                                          57705:
                                                                                                                                                                                                                                                                                                                                                                                                                            58825:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2191
2206
4264
4279
6647
6662
                                                                                                                                                                                                                                 52940
                                                                                                                                                                                                                                                                                                                                                    56031
                                                                                                                                                                                                                                                                                                                                                                                          57129
                                                                                                                                                                                                                                                                                                                                                                                                                            57706
                                        51354
                                                                            51531
                                                                                                                51938
                                                                                                                                                      52067
                                                                                                                                                                                             52221
                                                                                                                                                                                                                                                                         53796
                                                                                                                                                                                                                                                                                                             55051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC006895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC006895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC006895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
```

à

ö

Gaps

"LIPA2"

```
28853. .29041
/rpt_family="L2"
29215. .2937
/rpt_family="(TA)n"
complement(29601. .29878)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement(33538. 33697)
/rpt_family="MER63"
3837. 34328
/rpt_family="MER68"
35093. 35135
/rpt_family="AT_rich"
35426. 35488
/rpt_family="AT_rich"
37991. 38011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(19501. .19824)
/rpt_family="2".
complement(21666. .21766)
/rpt_family="12".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AT_rich"
complement(22499. .22852)
complement(22499. .22852)
frpt_family="rHEIC"
22855. .23102
/rpt_family="LiM4c"
/rpt_family="LiM4"
/rpt_family="LiM4"
/rpt_family="LiM4"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
/rpt_family="RER53"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="AT_rich"
complement(31797. .32050)
'rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omplement(28657. .28726)
rpt_family="MER5A"
8853. .29041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omplement(30090, .30704)
rpt_family="MLT21"
0811, .30840
rpt_family="A1_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7628. .27653
rpt_family="(TTA)n"
complement(27655. .27936)
rpt_family="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pt_family="L1M4"
mplement(26673. .26939)
pt_family="L2"
628. .27653
                                                                                                                                                                                                                       /rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family="Lipx"/rpt_family=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   807. .25837
pt_family="(GAAAA)n"
957. .26580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37991. .38011
/rpt_family="AT_rich"
                                                                                                                /rpt_family="AT_rich"
13879. .13923
/rpt_family="AT_rich"
14075. .14117
                                                                                                                                                                                           14075. 14117
/rpt_family="(TA)n"
14365. 14308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /531. .i/~~
rpt_family="AT_rich"
8835. .19103
               /rpt_family="(TA)n"
13756. 13824
                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="L1PA2" 7531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sass. .19103
rpt_family="MLT1K"
/rpt_family="AluSx"
13301. .13335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ytto. .ly442
'rpt_family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5. .31499
_family="A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                        repeat_region
                                                                                                                                                            repeat_region
                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                               repeat_region
         Hagos, B., Heaford, A., Horton, L., Howland, J.C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKenan, K., McLaughlin, J., Meldan, M., Morris, W., Morrow, J., Mychaleckyj, J., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Stanger-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Serge, S., Torruella-Millar, II., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.

Direct Submission

L. Submitted (29-JUL-1999) Whitehead Institute/MIT Center for Genome Submitted (29-JUL-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, WSA On Jul 29, 1999 this sequence version replaced 91:5542046.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, A., Linge, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .161449
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="hRPK:146_P_2"
/clone_lib="RPK:11 human BAC library"
/map="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="Mer9"
10920. 10980
/rpt_family="Cr-rich"
complement(1178. .11264)
/rpt_family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="L1MD1"
|2619. .12652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(TA)n"
complement(12996. .13300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MIR"
complement(3495..3674)
/rpt_family="MIR"
complement(4404..4514)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (810. 949)
/rpt_family="MER55"
1332 .1356
/rpt_family="AT_rich"
complement (1925. 2026)
/rpt_family="MER58"
2810. 2896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="AT_rich"
12761. 12787
/rpt_family="AT_rich"
12867. 12904
/rpt_family="AT_rich"
12910. 12995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="AT_rich"
complement(5930. .8561)
/rpt_family="Charlie3"
3589. .8612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="AT_rich"
9126. 9167
/rpt_family="AT_rich"
10187. ,10698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="AT_rich"
1638. .11702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1638. .11702
rpt_family="(TA)n"
.1920. .11947
rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rpt_family="AT_rich"
613. .8907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pt_family-"(CAT)n"
00. .5529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="AluSg"
908. .8918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sonrce
                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
```

```
Surface, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferrelra, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Aleaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKenan, K., McRens, T., Lehoczky, J., Levine, R., Ileu, C., Liu, G., Locke, K., Marquis, N., McEwan, P., McGurk, A., McRenan, K., McPheeters, R., Malquim, J., McEwan, P., McGurk, A., McKenan, K., McPheeters, R., Malquim, J., McEwan, P., McGurk, A., McKenan, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Peterson, K., Santcos, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramanian, C.H., Volan, M., X., Wyman, D., Ye, W.J., Zinmer, A. and Zody, M.

Lirell, A., Vassillev, H., Viel, R., Vo, A., Mu, X., Wyman, D., Ye, W.J., Zinmer, A. and Zody, M.

Lirell, A., Yassillev, H., Viel, R., Vo, A., Mu, X., Wyman, D., Ye, W.J., Zinmer, A. and Zody, M.

Lirella, A., Tesfaye, S., Green, P. (1996-1997)

Shit, A.F., & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG 19-JAN-2000
HOMO Sapiens chromosome 11 clone RP11-88122 map 11, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 161986)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 11, clone RP11-88122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 40; Length 161449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD 101906 CAATACCTGAAATCTTATTTTTTTTTTCGGAAAGTATAGGTTCTTCCATG 101856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CAAAAATTGAAATTTTATTTTTTTTTTTGGAATATAAAGCGGCCGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 30.2; DB; Pred. No. 66; 0; Mismatches
                   /rpt_family="(TG)n"
38618. 38915
38618. 38915
complement(40279. 40618)
/rpt_family="Mark468"
complement(40768. 41251)
/rpt_family="LiMA8"
41252. 41384
41303. 41388
                                                                                                                                                                                                                                                                   /rpt_family-"(TA)n"
complement(41390. 41557)
/rpt_family-"LIMA7"
41558. 41673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L1363
                                                                                                                                                                                                                                                                                                                                                                 41558. .41673
/rpt_family="(TA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC021672.1 GI:6716080
HTG: HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 161986)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 40.3%;
Best Local Similarity 74.5%;
Matches 38; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
repeat_region
                                                 repeat_region
                                                                                                                                                          repeat_region
                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
AC021672/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
```

ò

```
NOTE: This is a 'working draft' sequence. It currently consists of 35 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                          1708: contig of 1708 bp in length gap of unknown length of 1466 bp in length opposite of 1466 bp in length gap of unknown length opposite of 1469 bp in length gap of unknown length opposite of 1739 bp in length gap of unknown length langth of 1730; contig of 1739 bp in length gap of unknown length langth gap of unknown length ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown l
of 9948 b
unknown l
of 9051 b
Center clone name: 88_I_22
                                                                                                                                                                                                                                                                                                       1709
                                                                                                                                                                                                                                                                                                                                                      3195
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33758
                                                                                                                                                                                                                                                                                                                                                                                                        4664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81366
```

123090:

114040

```
AL121751.7 GI:6630762
                                                                                                                                                                                                          Ouery Match
Best Local Similarity 82.9%;
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lloyd, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSJ324017
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
HS1093G12/c
LOCUS
DEFINITION E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
FEATURES
                                                                                                                                                   ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Dec 11, 1999 this sequence version replaced gi:5881522. Bases 1-4149 of IGF clone F216 overlap with bases 91042-95190 of TAMU clone T10P12 (gb]AC007203) and an unknown number of bases overlap at the end of F216 overlap with IGF clone F28H19 (gb]AC006423).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tobases 1 to 108061)

Federspiel, N.A., Palm, C., J., Conway, A.B., Conn, L., Hansen, N.F., Faderspiel, N.A., Palm, C., J., Rowley, D., Buehler, E., Dunn, P., Altafi, H., Aramenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Gonzalez, A. Kremenetskala, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskala, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Suhmitted (11-DEC-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Hutzar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-AUG-1999) DNA Sequencing and Technology Center, Submitted (26-AUG-1999) DNA Sequencing Avenue, Palo Alto, CA 94304, Stanford University, 855 California Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC009526 108061 bp DNA PLN 11-DEC-19:
Arabidopsis thallana chromosome I BAC F2J6 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                           Length 161986;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                              13 others
         gap of unknown length 132651: contig of 9561 bp in length gap of unknown length contig of 12067 bp in length gap of unknown length 161986: contig of 17268 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGCCAAAAATTGAAATTTTTTTTTTTTTTGGAATATAAAG 43
                                                                                                                                                                                                                                                                   /clone_"RP11-88122"
/clone_lib="RPCI-11 Human Male BAC"
| 36630 c 35856 g 43893 t 13
                                                                                                                                                                                                                                                                                                                                                                                                    45;
                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
6
                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                  Score 30.2; DB; Pred. No. 66; 0; Mismatches
                                                                                                                                 Location/Qualifiers
1. .161986
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
/map="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 108061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC009526.3 GI:6560894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis.
1 (bases 1 to 108061)
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 81.4%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thale cress.
                                                                                 132652
                                        123091
                                                                                                                        144719
                                                                                                                                                                                                                                                                                                                       45594 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC009526
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                   FEATURES
```

õ

```
Direct Submission

Louding (21-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CBL0 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

CBL0 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Dec 22, 1999 this sequence version replaced gi:5562044.

IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in represent the release of this data is based on the understanding that the sequence may change as work continues. The sequence may contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00409 Length: 141655bp.

* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSJ324017 218305 bp DNA HTG 17-FEB-2000 HOMO sapiens chromosome 20 clone RP3-324017, *** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000
*** SEQUENCING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 122840 AAAAATGGAATATTTTTTTTTTTTAAAAAAAATATGCCAAGCTGGGCCAGGC 122784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 141655)
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 141655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AAAAIIGAAAIIIIAAITIIIIIIIIIIGGAAIAIAAAGCGGCCGCCAIGGGCCCGGC
                                                                                                                                                                                                                                                                     Length 108061;
                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                 4 others
                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS1093G12 141655 bp DNA HOMO sapiens chromosome 20 clone RP5-1093G12, PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                        -
DD 25278 GCTAAAAATGAAATTCAATTTTTTTTTTTGAAATTAA 25318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                         2 GCCAAAAATTGAAATTTTTTTTTTTTTGGAATATAAA 42
                                                                                                                                                                                                                                                                     .;
œ
Location/Qualifiers
1. 108061
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.7%; Score 29.8; I Best Local Similarity 70.2%; Pred. No. 85; Matches 40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                     Score 29.8; DE pred. No. 82; 0; Mismatches
                                                                                                                                                                 ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome-"20"
/clone-"RP5-1093612"
/clone_lib="RRCI-5"
39105 a 32980 c 31848 g 37722
                                                                                                                                        /clone="F2J6"
35398 a 19039 c 19111 g 34509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .141655
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIG; HIGS_PHASE1; HIGS_DRAFT
```

COMMENT

```
Search completed: May 29, 2000, 21:35:19
Job time: 36851 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-FBB-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonereques/Esanger.ac.uk
On Feb 19, 2000 this sequence version replaced g1:6983401.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, segments. Contig_ID: 00212 Length: 22806bp
Contig_ID: 00229 Length: 2485bp
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 218305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contig_ID: 03226 Length: 1158bp
Contig_ID: 03235 Length: 125bp
Contig_ID: 03242 Length: 2725bp
Contig_ID: 03251 Length: 26098bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124367 125166: gap of 1800 bp 125167 130719: contig of 553 bp in length 130720 131519: gap of 800 bp 131520 138618: contig of 7099 bp in length 138619 139418: gap of 800 bp 145242 145241: gap of 800 bp 145242 146322: contig of 1081 bp in length 14442 145241: gap of 800 bp 145242 146322: contig of 1081 bp in length 146321 148626: contig of 1504 bp in length 148627 149426: gap of 800 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65857 66656: gap of 800 bp 6657 89462: contlg of 22806 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92708 93507: gap of 800 bp
93508 94528: contig of 1021 bp in length
94529 9528: gap of 800 bp
95329 124366: contig of 29038 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65856: contig of 65856 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89463 90262: gap of 800 bp
90263 92707: contig of 2445 bp in length
PROGRESS ***, 24 unordered pieces.
                                                                                   AL110115.16 GI:7007308
HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138619 139418: gap of
139419 144441: contig
14442 145241: gap of
145242 146322: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124367 125166:
125167 130719
                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contigno
Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig_ID:
Contig_ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contig_ID:
Contig_ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contig_ID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contig_ID:
                                                                                                                                                                                                                                                                                                                                                                                                            Dunn, M.
                                                                                                                                                                       SOURCE
                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
```

```
Db 202922 AAAAATGGAATATTATTTTTTTTTTAAAAAAAAAAATATGCCAGGCCAGGC 202978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 218305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AAAATTGAAATTTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCCGGC
              15:034 15:1833; gap of 1800 bp 15:034 15:033 15:033: contig of 4240 bp in length 15:0574 15:0573: contig of 4240 bp in length 15:0574 15:0573: contig of 4248 bp in length 15:0576 15:058: gap of 10:09 bp in length 16:2150 16:2159: gap of 10:09 bp in length 16:228 16:7027: gap of 10:09 bp in length 16:028 16:027: contig of 10:09 bp in length 16:028 16:027: contig of 10:09 bp in length 16:028 16:027: contig of 10:09 bp in length 16:029 17:027: gap of 10:09 bp in length 17:0279 17:027: contig of 19:04 bp in length 17:0279 17:027: contig of 10:05 bp in length 18:028 18:089: contig of 12:05 bp in length 18:08 18:08 19:05 10:05 bp in length 18:08 18:08 19:05 10:05 bp in length 18:08 18:08 18:08 10:05 bp in length 18:08 18:08 19:05 10:05 bp in length 19:08 19:05 10:05 bp in length 19:08 19:05 10:05 bp in length 19:0207: gap of 10:05 bp in length 19:08 19:05 10:05 bp in length 19:08 19:05 10:05 pp in length 19:08 19:05 10:05 pp in length 19:05 pp in length 10:05 pp in length 19:05 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52311 t 18408 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.7%; Score 29.8; DB 33; 70.2%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches

    .218305
/organism="Homo sapiens"

σţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP3-324017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-3"
47647 c 48369 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 70.2
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51570
```

. .

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

May 29, 2000, 21:58:06 ; Search time 1446.77 Seconds (without alignments) 12.970 Million cell updates/sec Run on:

US-08-935-377-3 75 1 GGCCAAAAATTGAAATTTTA......GCCCGGCCGCCAACGGCGGA 75 Title: Perfect score: Sequence:

IDENTITY_NUC Gapox 10.0 Scoring table:

623170 Total number of hits satisfying chosen parameters:

311585 segs, 125096042 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	Chimeric virus con	Vir	Sequence of plasmi	ğ	ō	ĕ	ō	öţ	ŏ	ö	oter	ij	Sequence of plasmi	οŧ	ō	Sequence of clone	Human flavin-conta		sol1(	Coding sequence fo	const	CT317.	÷	Sequence of modifi	Human genome fragm	E	DNA encoding a hum	ß	. BRCAl modulator pr	ptococcus pn	-	-N-0	Human gene signatu
SUMMARIES	£ £	T78340	T78341	040300	041005	Q41004	067969	040295	040296	040299	041030	041025	040248	040249	040278	040250	040279	V57274	V36503	V37789	V58357	041029	V89886	T71761	041006	077192	T31290	X51745	V52449	V29063	V52284	708	4	T26771
	DB	-	-	Н					Н																								rН	H
	Query Match Length	84	86	6474	5472	6811	42	51	23	3878	46	62	88	92	97	134	4145	25464	2002	90	4093	42	126	3471	55	232	3095	1923	2453	3256	13425	16891	2436	238
ď	Query Match	3.	53.3	52.8	ä	ä	ö	50.7	50.7	50.7	36.0	36.0	36.0	36.0	35.5	35.5	35.5	35.5	₹.	34.4	4	34.1	33.9	33.9	33.6	33.6	33.6	33.3	33.3	33.3	33.3	33.3	33.1	32.8
	Score	40	40	39.6	8	œ.	38	38	38	38	27	27	27	27			26.6		26	ď.	25.8	S.	S.	'n.	S.	ď.	ů	25	25	25	25	~	24.8	٩.
	Result No.			c 3			v	7	ω υ		10	11	12	c 13	ч	15	16	c 17	18	19	20	~	c 25	~	24	~	c 26	~	28	c 29	30	31	c 32	33

ö

, , g

Human secreted pro Neocallimastix pat	Human transforming Sequence encoding	Fil Picket Wilder Prostate cancer as Prostate cancer as	EST clone BR733. N Human secreted pro Sequence encoding	Continuation (14 o ERAB protein codin
				_13
X00670 V07560	T05055 N80916	X39988 X39988 X39990	V87415 V34269 N50530	V21209 V60576
711	3288 5040	768 812	368 1296 5760	110000 981
ω ω	ص ص	ייליט	32.3	m 0
32	322	3 3 2	322	32.3
99	<b>ωω</b> ς	* 4 4	000	C 4
24.	224	 24 .	24.2 24.2 24.2	24.2
35	37	0 K 4	4 4 4 1 2 6	44
U	υυ	υυ		υ

## ALIGNMENTS

*tag=

```
/label- Vaccinia virus p7.5
/note ="starting with the p7.5 internal NdeI site
at posn. 1241"
1339. 1344
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 93-126461/16.
Modified eukaryotic cytoplasmic DNA virus prodn. - involves
                                                                                                                                                                                     /*tag= g
/label= vaccinia virus synthetic early/late
                                                                                                                                                                                                                                                                                                                                                                                    (IMMO ) IMMUNO AG.
Dorner F, Falkner FG, Pfleiderer M, Scheiflinger F;
                                                                                                                                        /*tag= f
/label= HIV-MN env gene
complement (3917. .3970)
                                                                                                                           complement (1259. .3916)
                                                                                                                                                                                                                          complement (3971. .4015)
/label- E. coli gpt
complement (861. .1245)
                                                                                                  /*tag= e
/label= HpaI site
                                                                                                                                                                                                                                                                 complement (4016.
                                                                                                                                                                                                                                                                                               /label- prz19R
                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                      25-AUG-1992; 021269.
26-AUG-1991; US-750080.
20-JUL-1992; US-914738.
                                                                                                                                                                                                                                                                                                                                                                                                             93-126461/16
                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                       misc_feature
                                                                                      misc_feature
                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                               AU9221269-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                        promoter
                 promoter
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                   Example 9; Page 14: 68pp; English.

Example 9; Page 14: 68pp; English.

A method has been produced for the production of recombinant eukaryotic cytoplasmic DNA viruses for vaccine production. The method involves cytoplasmic DNA viruses for vaccine into the genome of a eukaryotic inserting a construct DNA molecule into the genome of a eukaryotic cytoplasmic DNA virus, transfecting cells with the virus, and selecting a recombinant virus that does not contain the double selection marker cassette from the construct DNA. The DNA molecule preferably contains cone or more foreign DNA segments of a gene encoding an antigen of a one or more foreign DNA segments of a gene encoding an antigen of a packles. Surface antigen gene, HBV 81-82-8 surface antigen gene, tick-borne encephalitis prem gene or tick-borne compalities gene), and has a double selection marker cassette which is flanked by at least two direct repeat DNA sequences, where at least is flanked by at least two direct repeat DNA sequences on tick-borne cassette comprises a dominant selection marker gene (preferably the colour selection marker is the cassette comprises a dominant selection marker is the Escotion marker gene). The pressent sequence represents the oselp?

E. coli hph or gpt gene). The pressent sequence represents the oselp?

E. coli hph or gpt gene). The pressent sequence represents the oselp?

C fowlootide used in the construction of chimeric NA vaccinia and colour casetines, especially containing an attenuated live recombinant pox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                            Prodn. of recombinant eukaryotic cytoplasmic DNA viruses for vaccine prodn. - using novel construct contg. foreign DNA and double selection marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CCAAAAATTGAAATTTTATTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric virus construction oligonucleotide ose1P2. Recombinant eukaryotic cytoplasmic DNA virus; vaccine production; double selection marker; attenuated live pox virus; HIV; HBV; surface antigen gene; encephalitis; tick-borne; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                    Dorner F, Eibl J, Falkner F, Scheiflinger F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 1; Length 86;
Pred. No. 0.0012;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= b
/label= Linker I in rc orientation
complement (110. .860)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .55
/*tag= a
/label= prz19R
complement (56. .108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-1993 (first entry)
Sequence of plasmid pselP-gp160MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  040300/c
ID Q40300; Standard; DNA; 6474 BP.
AC Q40300; Anos (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.3%;
82.1%;
                                     T/8341 standard; DNA; 86 BP.
T/8341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 A;
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46; Conservative
                                                                                                                                                                         10-JUL-1995; 110727.
10-JUL-1995; EP-110727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                          (IMMO ) IMMUNO AG.
Antoine G, Dorner
WPI; 97-079382/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                          Synthetic.
EP-753581-A1.
                                                                 13-0CT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                      15-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cds
                            r78341/c
              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                        ò
```

.6474)

/*tag= h /label= linker II

```
Modified eukaryotic cytopiasmic DNA virus proof. - Involves

proplasmic DNA virus genome

Example; Pages 169-172; 206pp; English.

Cytoplasmic DNA virus genome

Example; Pages 169-172; 206pp; English.

Cytoplasmic DNA virus genome

Cytoplasmic DNA virus

Cytoplasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3964 AAAAATTGAAATTTTATTTTTTTTTGGAATATAAATAAGGCTCCATGGCC 3911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 52.8%; Score 39.6; DB 1; Length 6474; Best Local Similarity 83.3%; Pred. No. 0.0038; Andtches 45; Conservative 0; Mismatches 9; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAAAITGAAAITITAITITITITITITIGGAATATAAAGCGGCCGCCAIGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1410 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1532 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1648 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
Q41005/c
ID Q41005 standard; DNA; 5472 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o-Ncol and o-Nsil.
Sequence 6474 BP;
```

ö

*

7

Synthetic.

promoter

cds

promoter

```
"R ACTOUNTING AG.

NAME OF THE FAILURE FG, Pfleiderer M, Scheiflinger F;

NAME OF THE FAILURE FG, Pfleiderer M, Scheiflinger F;

NAME OF THE FAILURE FG, Pfleiderer M, Scheiflinger F;

NAME OF THE STATE OF THE FG OF THE STATE O
                                                                                                                                                                                                                                                                                                                                                                                                               promoter.
/note-"flanked by a NocI site and a fused Bgill/
BamH site. The NcoI site harbors the start
codon TAC".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- E. coli gpt
/note- "the ORF starts at posn. 5494 and ends at
posn. 5950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 51.2%; Score 38.4; DB 1; Length 6811; Best Local Similarity 97.5%; Pred. No. 0.0085; Matches 39; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-7AN-1995 (first entry)
Sequence of modified vaccinia promoter p7.5.
Recombinant replicable vaccinia virus; hepatitis; promoter;
                                                                                                                                                                                                                                                                                                                                                                                        /label= vaccinia virus synthetic early/late
                                                                                                  /*tag-a
/label- bluescript II SK- sequence
/label- 225
/*tag- b
/label- NotI site 1
complement (2226. .4938)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= h
/label= bluescript II SK- sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CCAAAAATTGAAATTTTTTTTTTTTTGGAATATAAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'label - vaccinia virus p7.5
                                                                                                                                                                                                                                                                                                 /label= Prot S
complement (4939. .4992)
Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
NotI site 2
                                                    Location/Qualifiers
1. .2217
                                                                                                                                                                                                                                                                                /*tag= c
/label= Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         067969; standard; DNA; 42 BP. 067969; 02-JAN-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4993. .5493
/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .6811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5494. .6127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-1993.
25-AUG-1992; 021269.
26-AUG-1991; US-750080.
20-JUL-1992; US-914738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                 misc_feature
                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                            Synthetic.
                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
067969
ID 067969
AC 067969
DT 02-389
DE Sequen
KW Recombi
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A CANDO 1 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 1932. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         site and a fused BglII/
harbors the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= f
/label= E. coll gpt
/note= "the ORF starts at posn. 4215 and ends at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.7%; Score 38.8; DB 1; Length 5472; 79.3%; Pred. No. 0.0062; 1ve 0; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label - vaccinia virus synthetic early/late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= h
/label= bluescript II SK- sequences
                                                                                                                                                                                      /*tag- a
/label= bluescript II SK- sequence
2218. .225
/*tag= b
/label= FIX sequence
complement (2226. .3659)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Noci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3714. .4214
/*tag= e
/label= vaccinia virus p'
4215. .4848
                                                                                                                                                                                                                                                                                                                                                                                                               complement (3660. .3713)
                       O2-AUG-1993 (first entry)
Sequence of plasmid pNZgpta-FIX.
Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g /label= NotI site 2 4857. .5522
                                                                                                                               Location/Qualifiers
1. .2217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-1993 (first entry)
Sequence of plasmid pN2-gptaProtS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "flanked
BamHI site. The
                                                                                                                                                                                                                                                                                                                                                              /*tag= c
/label= Prot S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q41004/c
ID Q41004 standard; DNA; 6811 BP.
AC Q41004
DT 02-AUG-1993 (first entry)
DE Sequence of plasmid pN2-gptaPr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  posn. 4671"
4849. .4856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon TAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 79.3°
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-AUG-1992; 021269.
26-AUG-1991; US-750080.
20-JUL-1992; US-914738.
Q41005;
O2-AUG-1993
                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU9221269-A
```

ö

Gaps

ö

S

RESULT

g

ô

```
o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q40299/c
                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MERAD W
នូខូខូខូខូ
                                                                                                                                                                       à
                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyuptasmit Dura villa yeluomic S. Example; Page 158; 206pp; English.

Example; Page 158; 206pp; English.

The synthetic early/late promoter selp was used to express the The synthetic early/late promoter selp was used to express the The synthetic early/late promoter of the plasmid prw3 was substituted the O.6kb xbar-clai adaptor fragment of the plasmid as substituted by an Xbal-clai adaptor fragment of the plasmid do oligonucleotide o-542 and o-544. The intermediate plasmid coligonucleotide o-542 and o-544. The intermediate plasmid Aatii-Sphi fragment were substituted by the Aatii-Sphi adaptor fragment were substituted by the Aatii-Sphi adaptor fragment consisting of the annealed oligonucleotide o-541 and fragment was treated with Klenow-polymerase and inserted between the Puli sites of the plasmid pr219k. The resulting plasmid was called pr2-L2. The 0.6kb Clai-Nool fragment (the called pr2-L2. The 0.6kb Clai-Nool fragment (the T7-promoter-EMC-sequence) was replaced with a synthetic promoter fragment consisting of the annealed oligonucleotide o-selpi and
                                                                                                                                                                                                  Listuage (143) of accepting sequences were subcloned and engineered so as to be transcriptionally controlled by a engineered so to be transcriptionally controlled by a engineered so to be transcriptionally controlled by a confine or vaccinia-like promoter. A strong vaccinia promoter or procession of the HBV sequences or sequence in Q67967, can be one of several vaccinia or vaccinia or vaccinia or vaccinia to promoter used to direct expression of the HBV sequences. Ithe promoter used to direct expression of the HBV sequences. Ithe promoter of vaccinia polypeptide of 7.5 kD. Another vaccinia promoter, pli, in nature directs expression of vaccinia structural promoter, pli, in nature directs expression of vaccinia structural promoter, pli, in nature directs expression of vaccinia structural content of 11 kD. Unlike p7.5, pli is active only late in viral promoter (Q67969) is a strong synthetic promoter that is active in both early and late viral replication. Its sequence is partly considered on the p7.5 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                      Prevention and treatment of hepatitis - using recombinant replicable vaccinia viruses contg. hepatitis B virus surface and core antigen nucleotide sequences
Disclosure; Fig 6; 252pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Donner F. Falkner FG, Pfleiderer M, Scheiflinger F; WPI; 93-12646/1/16
Modified eukary/lic cytoplasmic DNA virus prodn. - involves direct molecular cloning of modified DNA molecule contg. cytoplasmic DNA virus genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
   prevention; therapy; epitope; hepatitis B virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            21 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 38; DB 1;
Pred. No. 0.0038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AAAAATTGAAATTTTTTTTTTTTTGGAATATAAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Souw PTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 50.7%; Score 38; DB 1 Similarity 100.0%; Pred. No. 0.0 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              4 G;
                                                                                                               Okeefe RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                ပ်
၀
                                                              09-JUN-1994.
25-NOV-1993; U11474.
25-NOV-1992; US-982211.
(ITBI-) INT BIOTECHNOLOGY LAB_INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q40295 standard; DNA; 51 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU9221269-A.
04-MAR-1993.
25-AUG-1992; 021269.
26-AUG-1991: US-750080.
20-JUL-1992: US-914738.
(IMMO ) IMMUNO AG.
                                                                                                                      Lewis T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                   Bernstine EG, Lew
WPI; 94-200247/24
                                                       09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
Q40295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Well; 93-120401/L0.

Well; 93-120401/L0.

Modified cukaryotic cytoplasmic DNA virus prodn. - involves
direct molecular closing of modified DNA molecule contg.

Cytoplasmic DNA virus genome
cytoplasmic plantal.

Cytoplasmic plantal.

Cytoplasmic dearly/late promoter selp was used to express the
cytoplasmic carly/late promoter fragment of the plasmid prism was substituted
by an Xbal-Clai adaptor fragment of the plasmid of the annealed
cytomorlectide o-542 and o-544. The intermediate plasmid
cragment consisting of the annealed by the Aatil-Sphi adaptor
fragment consisting of the annealed oligonuclectide o-541 and
costs. The resulting plasmid was called plz. The Xbal-Sphi
coststing of the plasmid prisms. The resulting plasmid was
called prz-Liz. The 0.6kb Clai-Nocl fragment (the
Ty-promoter-EMC-sequence) was replaced with a synthetic promoter
Cytopmoter-EMC-sequence) was substituted by the sall-Ndel adaptor
Cytopmoter-EMC-Sequence)
Cytopmoter-EMC-Sequence)
Cytopmote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                            ;
;
o-selPII. The 239pp SaII-NdeI fragment of the resulting intermediate plasmid was substituted by the SalI-NdeI adaptor consisting of the annealed oligonucleotides o-830 and o-857. resulting plasmid was called pselP-gpt-L2. Sequence 51 BP; 18 A; 4 C; 6 G; 23 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-AUG-1993 (first entry)
Sequence of oligo o-selPII of a synthetic promoter fragment. Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.7%; Score 38; DB 1; Length 53; 100.0%; Pred. No. 0.004; Pred. No. 1004; Pred. No. 1004; Namatches 0; Indels
                                                                                                                                                                                                                                                                                                            50.7%; Score 38; DB 1; Length 51; 100.0%; Pred. No. 0.004; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1993.
25-ANG-1992; 021269.
26-ANG-1991: US-750080.
20-JUL-1992; US-914738.
(IMMO ) IMMUNO AG.
WPI; 93-126461/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 AAAAATTGAAATTTTTTTTTTTTTTAAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AAAAATTGAAATTTTTTTTTTTTTAAA 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resulting plasmid was called pselp-gpt-L2. Sequence 53 BP; 24 A; 6 C; 4 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q40299;
02-AQG-1993 (first entry)
sequence of plasmid pselP-gpt-L2.
Plasmid; cloning; restriction site; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q40299 standard; DNA; 3878 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  040296 standard; DNA; 53 BP. Q40296;
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local'Similarity
Matches 38; Conserva
```

prp-Zsart construction oligomer #2.

Fowl pox virus; FPV: P2; promoter; vaccina virus; VV; mutation; apoAI; multiple cloning site; plasmid; thymidine kinase; tk; Marck's disease; intergenic region; post-translational modification; factor II; apoAII; factor V; factor VII; factor XII; factor IX; tick-borne encephalitis; hepatitis E; factor XII; factor XII; factor XIII; protein C; protein S; von Millebrand factor; hepatitis B; hepatitis C; malaria; plasminogen; apoAIIpo protein, viral antigen; infectious bronchitis; TBE; tetanus; HIV; HSV; pertussis; Newcastle disease; vaccine; ss.

Q41030 standard; DNA; 46 BP

(first entry)

29-JUL-1993

04-WAR-1993. 10-JUL-1992; 019580. 26-AGC-1991; EP-114300. (IMMO ) IMMUNO AG. DOTHER F, FELKHEF FG, Schefflinger F; WPI; 93-126452/16.

Synthetic.

1

```
RESULT
Q41030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Well; 3-1.2091/10.

Well; 3-1.2091/10.

Wolfifed eukaryotic cytoplasmic DNA virus prodn. - involves direct molecular cloning of modified DNA molecule contg.

Tytoplasmic DNA virus genome

Example; Pages 165-167; 206pp; English.

Example; Pages 165-167; 206pp; English.

C plog-gene of the HIV-1 MN strain. For the construction of pl2

The synthetic early/late promoter selp was used to express the gp160-gene of the HIV-1 MN strain. For the construction of pl2

The O.6bx Xbal-Clal fragment of the plasmid pring was substituted by an Xbal-clal adaptor fragment consisting of the annealed oligonucleotide o-542 and o-542 and o-544. The intermediate plasmid cangent consisting of the annealed oligonucleotide o-541 and cangent consisting of the annealed oligonucleotide o-541 and cangent was treated with Klenow-polymerase and inserted between the Poull sites of the plasmid pr219R. The resulting plasmid was called pl2. The xbal-sphin the Poull sites of the plasmid pr219R. The resulting plasmid was called pl2.-i.2. The Chromoter-EMC-called pl22. The O-68k Clal Nool fragment was treated with Rienow-polymerase and inserted between the Poull sites of the plasmid pr219R. The resulting plasmid was called pl22.-i.2. The O-68k Clal Nool fragment was treated with Rienow-polymerase and inserted between the Poull sites of the plasmid pr219R. The resulting plasmid was called pl22.-i.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The 239bp SalI-NdeI fragment of the resulting intermediate plasmid was substituted by the SalI-NedI adaptor consisting of the annealed oligonucleotides o-830 and o-857. The resulting plasmid was called pselP-gpt-L2.
                                                                                                                                                                                                                           /*tag= d
/label- Vaccinia virus p7.5
/note ="starting with the p7.5 internal NdeI site
at posn. 1241"
1339. .1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence) was replaced with a synthetic promoter fragment consisting of the annealed oligonucleotide o-selPI and o-selPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label vaccinia virus synthetic early/late
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMMO ) IMMUNO AG.
Dorner F, Falkner FG, Pfleiderer M, Scheiflinger F;
WPI; 93-126461/16.
                                                                                                             /*tag= b
/label= Linker I in rc orientation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           974 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.7%; Score 38; DB 1;
100.0%; Pred. No. 0.0099;
ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                            /*tag= g
/label= multiple cloning site
                                                                                                                                                                                                                                                                                                                       /*tag= e
/label= HpaI site
complement (1259. .1322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             927 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tay- )
/label= linker II
complement (1415. .3878)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (1375. .1414)
                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1323. .1374)
                                                                                                                                                                            / Label - E. coli gpt
complement (861. 1245)
                                                                                                                                                  complement (110. .860)
                                                                                            complement (56. .108)
                 .ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= k
/label= pT219R
                                                                          /label- pT219R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1012 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1991; US-750080.
20-JUL-1992; US-914738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1993.
25-AUG-1992; 021269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3878 BP;
                                     misc_feature
                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
```

```
29-JUL-1993 (first entry)
Pl promoter mutant sart.
Fowl pox virus; FPV; Pl1; promoter; vaccina virus; mutation; apoAI;
multiple cloning site; plasmid; thymidine kinase; tk; Marck's disease;
intergenic region; posptranslational modification; factor II apoAII;
factor V; factor VII; factor VIII; factor IX; tick-borne encephalitis;
factor X; factor XII; factor XIII; protein C; protein S; VV;
von Willebrand factor; hepatitis B; hepatitis C; hepatitis E; malaria;
plasminogen; apolipo protein; viral antigen; infectious bronchitis;
FBE; tetanus; HIV; HSV; pertussis; Newcastle disease; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Construction of the first than pox virus (FPV) P2 promoter sequence (see 041013 and 041018-20), multiple cloning sites (see 041015-16), the FPV thymidine kinase (tk) gene and the tk gene intergenic region (see also 040101-12). The P2 promoter belongs to one of the strongest natural promoters in vaccina virus (VV) infected cells. These plasmids may be used to express foreign proteins which require post-translational modification eg. Factors II, V, VII, VIII, X, X, XI, XII, XIII, proteins C and S, von Willebrand factor, plasminogen and derivatives, apolipo proteins, eg. apoAI and apoAII, and viral antigens, eg. hepatitis B- antigens and the antigens of hepatitis C and E viruses, of tickborne encephalitis (TBE) virus, antigens of HIV, HSV and whole or partial sequences of antigens which cause pertussis, infectious bronchitis, tetanus, malaria, Marck's disease and Newcastle disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 39; 92pp; English.
The sequences given in Q41027-45 are oligomers which were used in the construction of the insertion plasmids of the invention. These
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                         Prepn. of recombinant fowl pox virus for e.g. expression of proteins - by inserting foreign DNA into enlarged inter-genic region so FPV TK-gene remains intact and codes for entire thymidine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.0%; Score 27; DB 1; Length 46; llarity 85.7%; Pred. No. 6.5; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITIATITITITITITIGGAATATAAAGCGGCCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 TITITITITITITIGGCATATAATAGGCTGC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        these antigens being useful as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q41025 standard; DNA; 62 BP.
Q41025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
ö
```

ö

Gaps

ö

1368 AAAAATTGAAATTTTTTTTTTTTTTGGAATATAAA 1331

AAAAATTGAAATTTTATTTTTTTTTGGAATATAAA 42

S

à

셤

Query Match Best Local Similarity 100. Matches 38; Conservative

Length 3878; 0; Indels

Length 88;

```
04-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                   à
                                                                                                                         ద
                                                                                                                                                                                                                                                          Disclosure; Fig 18; 92pp; English.

Disclosure; Fig 18; 92pp; English.

Disclosure; Fig 18; 92pp; English.

The sequences given in Q41021-25 represent mutations of the vaccinia visus (VV) P11 promoter sequence which were included in the expression visus (VV) P11 promoter. Sequence which were included in the expression plannids of the invention. The sequences were unclear when given in the specification and so represent the "best guess" of sequence. These cases of this parallel surther comprised multiple cloning sites (see Q41015-16), the plannids further comprised multiple cloning sites (see Q41015-16), the also Q41011-12. These plasmids may be used to express foreign (see also Q41011-12). These plasmids may be used to express foreign (see covered to the virial virial virial virial sequence of antigens and factor, plasminogen and derivatives, apolipo proteins, eg. apohl and factor, plasminogen and derivatives, apolipo proteins, eg. apohl and separatish antigens of tick borne encephalitis (TBE) virus, of hepatitis C and E viruses, of tick borne encephalitis (TBE) virus, cause pertussis, infectious bronchitis, tetanus, malaria, Marck's disease and Newcastle disease, these antigens being useful as vaccines. Sequence 62 BP; 14 A; 4 C; 11 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified eukaryotic cytoplasmic DNA virus prodn. - involves Modified eukaryotic cytoplasmic DNA virus genome cytoplasmids pA1-52 and pA2-52 comprise gene expression cassettes plasmids pA1-52 and pA2-52 comprise gene expression cassettes prisablation start codon with a synthetic poxvirus promoter (S2), prior to direct molecular transfer into vaccinia virus vector vdTK by forced clouning. The S2 promoter is present in different orientations in the two plasmids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning
site of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
/*tag= a
/note= "yaccinia virus late promoter consensus
                                                                                                                                           Donner F. Falkner FG, Scheiflinger F;
WPI: 93-126452/16.
Preph of recombinant fowl pox virus for e.g. expression of proteins - by inserting foreign DNA into enlarged intergenic region so FPV TK-gene remains intact and codes for entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of plasmid pA1-S2 which comprises a first master sequence of plasmid pA1-S2 which comprises a first master site comprised of unique sites of a second master cloning the vaccinia virus vector designated vdTK with a poxvirus operatively linked to the first master cloning site. Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.0%; Score 27; DB 1; Length 62; 85.7%; Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dorner F, Falkner FG, Pfleiderer M, Scheiflinger F; WPI; 93-126461/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 TITIATITITITITIGGAATATAAAGCGGCCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 TTTTTTTTTTTTTTTGCATATAATAGGCTGC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q40248 standard; DNA; 88 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1993.
25-AUG-1992; 021269.
26-AUG-1991; US-750080.
20-UUL-1992, US-914738.
(IMMO ) IMMUNO AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.0%
Best Local Similarity 85.7%
Matches 30; Conservative
                                           sednence,
                                                                                                                 26-AUG-1991; EP-114300.
                                                                                04-MAR-1993.
10-JUL-1992; 019580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by forceu ...
orientations in the
                                                                                                                                       (IMMO ) IMMUNO AG.
                                                                                                                                                                                                                                               thymidine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
AU9221269-A.
                                                              AU9219580-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  å
```

ţ

```
Gaps
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified eukaryotic cytoplasmic DNA virus prodn. - involves Modified eukaryotic cytoplasmic DNA Airus genome cytoplasmic DNA Virus genome cytoplasmic DNA Virus genome cytoplasmic DNA Virus genome claim 63; Page 140; 206pp; English.

Plasmids pAl-S2 and pA2-S2 comprise gene expression cassettes suitable for association of open reading frames already having a suitable for association of open reading frames already having a translation start codon with a synthetic poxvirus promoter (S2), prior to direct molecular transfer into vaccinia virus vector vdTK by forced cloning. The S2 promoter is present in different sorientations in the two plasmids.

Sequence 92 BP; 37 A; 20 C; 14 G; 21 T;
                                                                                                                                                                                                                                                                                                                                                                                                  02-AuG-1993 (first entry)
Sequence of plasmid pA2-S2 which comprises a first master cloning
site comprised of unique sites of a second master cloning site of
the vaccinia virus vector designated vdTK with a poxvirus promoter
operatively linked to the first master cloning site.
Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dorner F. Falkner FG, Pfleiderer M, Scheiflinger F;
Dorner F. Falkner FG, Pfleiderer M, Scheiflinger F;
WPI; 93-126461/J6.
Modified eukaryotic cytoplasmic DNA virus prodn. - involves
direct molecular cloning of modified DNA molecule contg.
Cytoplasmic DNA virus genome
Example; Page 153; 206pp; English.
Plasmids pN2gpt-S3A and pN2gpt-S4 comprise expression cassettes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-Aug-1993 (first entry)
Sequence of synthetic linker consisting of the oligonucleotide
P-artp(9) abd P-artp(10) used ot construct pN2gpt-S4.
Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%; Score 27; DB 1; Length 92; 85.7%; Pred. No. 7.5; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMMO) IMMUNO AG.
36.0%; Score 27; DB 1;
85.7%; Pred. No. 7.4;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 TITIAITITITITITIGGAATATAAAGCGGCCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50
                                                                                                                                                                 16 TITIAITITITITITGGAAIATAAAGCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
040278/-
AC 040278 standard; DNA; 97 BP.
AC 040278;
DT 02-AUG-1993 (first entry)
DE Squence of synthetic linker or
DE Partp(9) abd P-artp(10) used of
NW Plasmid; cloning; restriction is
Synthetic.
PN AU9221269-A.
PD 04 WAR-1992;
DF 25-AUG-1992; US-9175080.
PR 26-AUG-1991; US-750080.
PR 26-AUG-1991; US-750080.
PR 26-AUG-1991; US-750080.
PR 26-AUG-1992; US-914738.
PA (IMMO) IMMUNO AG.
PI Dorner F, Falkner FG, Pfleid DR WPL; 93-1264601/16.
DR WPL; 93-1264601/16.
DR MOGHIED GURARDOLLO CYtoplasmit PT Glorid Gurardollar cloning of mo Cytoplasmit Charact Molified Gurardollar cloning of mo F Cytoplasmic Page 153; 206Pp; Engle CC Plasmids PAG9Pt-53A and pN2gpt-53A and PN2gpt
                                                                                                                                                                                                                                                                                                                     040249/c
ID 040249 standard; DNA; 92 BP.
AC 040249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30; Conservative
            Query Match
Best Local Similarity 85.77
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAK-1992; 021269.
25-AUG-1991; US-750080.
26-AUG-1992; US-914738.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dorner'F, Falknes
WPI; 93-126461/16
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dorner F, Falkner FG, Pfleiderer M, Scheiflinger F;

WPI: 93-126461/16.

WPI: 93-126461/16.

Modified eukaryotic cytoplasmic DNA virus prodn. - involves
direct molecular cloning of modified DNA molecule contg.

Cytoplasmic DNA virus genome

S Claim 58; Page 141; 206pp; English.

Claim 58; Page 141; 206pp; English.

C laim 58; Page 141; 206pp; English.

C comprises cleavage site that is unique in the plasmid with a Notic endonuclease cleavage site that is unique in the plasmid with a Notic site at each end. In this plasmid the DNA segment may further

C comprises a selective marker gene under transcriptional control of a poxvirus promoter. for instance pN2-spta and pN2-sptb. The DNA segment may further comprise a second poxvirus promoter operatively

C linked to a DNA sequence comprising a restriction endonuclease cleavage site, e.g. pN2gpt-54 are comprised of gene expresson cassettes suitable for association of an open reading frame having a translation start codon, with a synthetic
with a selective marker. These plasmids were constructed by first making plasmids plasmid plasmid virus pr. 5 promoter, flanked by several unique restriction sites including Noti. For the construction of plasmid plaspt-S3A, the parental plasmid plasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter S4 prior to direct molecular transfer into a unique site in vaccinia virus vectr vorts (26 A; 34 C; 35 A; 34 C; 35 A; 36 A; 36 A; 37 A; 38 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-AUG-1993 (first entry)
Sequence of a DNA segment comprising a sequence-specific
Sequence of a DNA segment comprising a sequence-specific
endonuclease cleavage site with a cleavage site for the bacterial
restriction endonuclease NotI at each end and a selective marker
gene and a second poxylus promoter in plasmid pN2-gpt-S4.
Plasmid; cloning; restriction site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TITIATITITITITITIGGAATATAAAGCGCCCCCCATGGGCCCGGCCGCCAACGC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26.6; DB 1; Length 134; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26.6; DB 1; Length 97;
Pred. No. 9.9;
0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q40250 standard; DNA; 134 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.5%;
Best Local Similarity 66.7%;
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 66.7
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
AU9221269-A.
04-MAR-1993.
25-AUG-1992; US-750080.
26-AUG-1992; US-750080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IMMO) IMMUNO AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                040250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 040250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
```

85

16 TITIATITITITITITIGGAATATAAAGCGGCCGCCATGGGCCCGGCCGCCAACGGC 72

දු ද

29 TITITITITITITITITIGGGATATAAATCGTTAACGAATTCCATGGCCCGGGAAGGC

Search completed: May 29, 2000, 21:58:11 Job time: 38159 sec

,

us-08-935-377-3.rni

```
, CLONE: sart(4)
US-08-232-463-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                             υU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113, App
113, App
13, Appli
11, Appli
11, Appl
11, Appl
11, Appl
10, Appl
19, Appl
                                                                                                                                                                         May 29, 2000, 22:08:49 ; Search time 621.83 Seconds (without alignments) 15.678 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12, Appl
18, Appl
20, Appl
11, Appl
11, Appl
12, Appl
38, Appl
39, Appl
39, Appl
31, Appl
31, Appl
31, Appl
31, Appl
31, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Note of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                      75
1 GGCCAAAATTGAAATTTTA......GCCCGGCCGCCAACGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgnl_6/ptodata/1/ina/5A_COWB.seq:*
/cgnl_6/ptodata/1/ina/5B_COWB.seq:*
/cgnl_6/ptodata/1/ina/5C_COWB.seq:*
/cgnl_6/ptodata/1/ina/5D_COWB.seq:*
/cgnl_6/ptodata/1/ina/c_COWB.seq:*
/cgnl_6/ptodata/1/ina/PCTUS_COWB.seq:*
/cgnl_6/ptodata/1/ina/PCTUS_COWB.seq:*
/cgnl_6/ptodata/1/ina/PCTUS_COWB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-232-463-40
US-08-232-463-40
US-07-750-080A-11
US-07-750-080A-12
US-07-750-080A-13
US-08-747-121-20
US-08-747-121-20
US-08-747-121-20
US-08-747-121-1
US-08-748-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                       nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                   US-08-935-377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834
834
2058
3288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . . . . . . . . .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
27
27
27
27
26 . 6
26 . 6
26 . 6
                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                          OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             000
```

```
C 27 23.8 31.7 49 6 PCT-US96-09848-20 Sequence 20, Appl 23.8 31.7 55 1 US-07-803-633A-3 Sequence 3, Appl 23.8 31.7 55 1 US-07-803-633A-4 Sequence 4, Appl 23.8 31.7 55 3 US-08-525-742-13 Sequence 14, Appl 32 23.8 31.7 70 3 US-08-95-554A-43 Sequence 14, Appl 34 23.8 31.7 70 3 US-08-97-554A-43 Sequence 43, Appl 34 23.8 31.7 74 3 US-08-097-554A-44 Sequence 44, Appl 35 23.8 31.7 74 3 US-08-097-554A-44 Sequence 44, Appl 36 23.8 31.7 74 5 US-08-040-44 Sequence 44, Appl 36 23.8 31.7 74 5 US-08-040-44 Sequence 44, Appl 36 23.8 31.7 74 5 US-08-525-742-51 Sequence 51, Appl 51 3 US-08-525-742-51 Sequence 20, Appl 52 23.8 31.7 93 3 US-07-750-0804-40 Sequence 20, Appl 54 23.8 31.7 95 3 US-08-525-742-29 Sequence 20, Appl 54 23.8 31.7 102 1 US-07-540-10 Sequence 10, Appl 54 23.8 31.7 102 1 US-08-525-742-10 Sequence 10, Appl 54 23.8 31.7 102 5 US-08-40-10 Sequence 10, Appl 54 23.8 31.7 102 5 US-08-040-10 Sequence 10, Appl 54 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-60-10 Sequence 10, Appl 55 23.8 31.7 102 5 US-08-60-60-10 Sequence 10, Appl 55 23.8 31.7 102
```

## ALIGNMENTS

```
Sequence 40, Application US/08232463
Sequence 40, Application US/08232463
Patent No. 5670367
EAPPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER: 52
CORRESPONDENCE: 52
CORRESPONDENCE: 52
CORRESPONDENCE: 52
CORNERY: US
COUNTRY: US
CONNURY: US
CONNURS: US
C
```

```
Sequence 12, Application US/07750080A
Patent No. 5445953
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: EURAROTIC CYTOPLASMIC DNA VIRUS GENOME
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: BUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME
TOWNER OF SEQUENOES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FILING DATE: 19910826
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BERY. Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/106 IMMU
TELEPHONE: (703)836-9300
TELEPHA: (703)836-9300
TELEPHA: (703)836-9300
TELEPHA: (703)836-9300
TELEPHA: (703)831-109
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TITIATITITITITIGGAATATAAAGCGGCCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27;
Pred. No. 1
                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 22313-0299
COMPUTER.READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-042>
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CLONE: pAl-S2 (Fig. 4.5) US-07-750-080A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.77
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 88 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:, USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-07-750-080A-12/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 27; DB 1; Length 63; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Score 27; DB 1; Length 46;
Pred. No. 1.6;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                       Sequence 47, Application US/08232463
Sequence 47, Application US/08232463
Patent No. 5670367
Patent No. 187037
Patent No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 TITTATITITITITGGAATATAAAGCGGCCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 TITITITITITITITITITGGCATATAATAGGCTGC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                            16 ITTIATTITITITITGGAATATAAAGCGGCCGC 50
                                                                                                                                                                30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT. Stephen A.
REFERENCE/DOCKET NUMBER: 29.768
REFERENCE/DOCKET NUMBER: 30472/114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/07750080A Patent No. 5445953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.0%;
85.7%;
   Query Match 36.0%;
Best Local Similarity 85.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 85.7
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 63 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CLONE: sart
US-08-232-463-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-07-750-080A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                    g
                                                                                                                                            ò
```

Gaps

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
US-07-750-080A-41/C

| Sequence 41, Application US/07750080A
| Patent No. 5445953
| CENERAL INFORMATION:
| APPLICANT: DORNER, F. |
| APPLICANT: FALKNER, F. G. |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED |
| TILLE OF INVENTION: DIRECT MOLECULAR CLONING OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 TITIAITITITITITIGGAATATAAAGCGGCCGCCATGGGCCCGGCCGCCAACGGC
                                                                                                                                                                                                                                                                                                                                                                                                   Score 27; DB 1; Length 9890;
Pred. No. 7.9;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 35.5%; Score 26.6; DB 1; Length 97; Best Local Similarity 66.7%; Pred. No. 2.7; Matches 38; Conservative 0; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FILING DATE: 19910826
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/106 IMMU
TIBLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4326 TITITITITITITITITITICCATATAAATAGGCTGC 4292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TITITATITITITITIGGAATATAAAGCGCCCC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: P-artP(10)
   INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 9890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                   36.0%;
ilarity 85.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: ('C')
TELEFAX: 899149
TELEX: 899149
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 97 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                  : IMMEDIATE SOURCE:
CLONE: pTZgpt-sart
US-08-232-463-18
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-750-080A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FILING DATE: 19910826
CLASSIFICATION: 435
ACTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/08232463
Patent No. 5670367
CEMERAL INFORMATION:
APPLICANT: BONEE, F.
APPLICANT: SCHEIFLINGER, F.
TILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
INTLE OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 27; DB 1;
Pred. No. 2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 TITIAITITITITITIGAATATAAAGGGGCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ririririririririsecararaarageciec 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA CCUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (703)836-9300
TELEX: 899149
INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS: LENGTH: 92 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 85.7%;
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CLONE: pA2-S2 (Fig. 4.5)
US-07-750-080A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-18/c
```

ò g

셤

```
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                   STREET: 1155 Av
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-747-121-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 TITIAITITITITITIGGAATALAAAGCGGCCGCCATGGGCCCGGCCGCCAACGGC 72
        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/08747121
Patent No. 5974290
GENERAL INFORMATION:
APPLICANT: Murphy, Gerald
APPLICANT: Boynton, Alton
APPLICANT: Sengal, Anil
TITLE OF INVENTION: NOCLEOTIDE AND AMINO ACID
TITLE OF INVENTION: SEQUENCES OF A D2-2 GENE ASSOCIATED WITH
TITLE OF INVENTION: BRAIN TUMORS AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                   APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: EUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FILING DATE: 19910826
CLASSITCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT Stephen A.
REGISTRATION NUMBER: 29,768
REFIRENCE/DOCKET NUMBER: 30,778
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
35.5%; Score 26.6; DB
Best Local Similarity 66.7%; Pred. No. 2.9;
Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                           STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                  Sequence 14, Application US/07750080A Patent No. 5445953 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic); IMMEDIATE SOURCE:
CLONE: PN2gpt-S4
US-07-750-080A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-747-121-20
                                                                                                                     US-07-750-080A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 TITIAIIITITITITIGGAATATAAAGCGGCCGCCATGGGCCCGGCCGC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
34.7%; Score 26; DB 3
Best Local Similarity 70.0%; Pred. No. 8.2;
Matches 35; Conservative 0; Mismatches
                                       COMPUTER: NEADABLE FORM.

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OOPENATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,121
FILING DATE: 09-NOV-1996
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: 15
FILING DATE: 09-NOV-1996
CLASSIFICATION NUMBER: 31,232
ATORNEY/AGENT INFORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REGISTRATION NUMBER: 8511-008
TELEPHONE: (212)790909
TELEPHONE: (212)790909
TELEPAX: (212)869864
TELEPAX: (212)869864
TELEPAX: (212)869811CS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                        LENGIH: 1000 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2711
```

```
RESULT 11
US-07-750-080A-38
: Sequence 38, Application US/07750080A
: Patent No. 5445953
: GENERAL INFORMATION
: APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: DIRECT MOLECULAR CLONING GENOME
NUMBER OF SEQUENCES: 42
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Foley & Lardner
: STREET: 1800 Diagonal Road, Suite 500
: CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-07-750-080A-39/C
US-07-750-080A-39/C
Sequence 39, Application US/07750080A
Patent No. 5445953
Sendence 30, Application US/07750080A
PAPPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKER, F. G.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: BUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 55
16 TITIAITITITITITIGGAATATAAAGCGGCCGCCAIGGGCCCGGCCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: USA
Z119: 22313-0299
ZIP: 22313-0299
COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OFFWARE: PATEMIT Release #1.0, Version #1.25
SOFTWARE: PATEMIT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FLING DATE: 19910826
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
RESTSTRATION NUMBER: 29,7683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

33.6%; Score 25.2; DB 1;
Best Local Similarity 90.0%; Pred. No. 6.1;
Matches 27; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 ITTTATTTTTTTTTGGAATATAAAGCG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 TITITITITITITITITICCATATAAATCG 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEFAM: (703)683-4109
TELEFAM: 899149
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: P-artP(11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-07-750-080A-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ğ
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
US-08-715-568A-2/C
; Sequence 2, Application US/08715568A
; Petent No. 5856463
; GENERAL INFORMATION:
    APPLICANT: Prydz, Hans Peter Blankenborg
    APPLICANT: Brede, Gaute
    TITLE OF INVENTION: Treatment
    TITLE OF INVENTION: Treatment
    NUMBER OF SEQUENCES: 14
    CORRESPONDENCE ADDRESS: 14
    CORRESPONDENCE ADDRESS: 14
    CORRESPONDENCE ADDRESS: 15
    STREET: 600 South Avenue West
    CITY: Westfield
    STREET: NJ
    COMUTRY: USA
    COMUTRY: USA
    COMPUTER: EMP PC Compatible
    COMPUTER: IBM PC Compatible
    COMPUTER: BATENTING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PS PETENTIN Release #1.0, Version #1.25
    CURRENT APPLICATION NUMBER: US/08/715,568A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 3471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1021 TITIGITITITITITIAGACAGAGACCCCCTCGTCGCCCCAGCCCC 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 ITITATITITITITIGGAATATAAAGCGGCCGCCATGGGCCCGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25.4; DE Pred. No. 18; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.7%; Score 26; DB Best Local Similarity 70.0%; Pred. No. 10; Matches 35; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FOLEY, Shawn P.
REFERENCE/DOCKET NUMBER: FORSK 3.0-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-654-5000
                                                                                                                     8511-008
                   FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME: Baldwin, Geraldine F
REGISTRATION NUMBER: 31,232
REFRENCE/DOCKET NUMBER: 8511-
TELECHONICATION INFORMATION:
TELEFAX: (212)7909090
TELEFAX: (212)869864
TELEFAX: (6141 PENNIE
INFORMATION FOR SEO ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 2002 base pairs
TYPE: nucleic acid
STRANBENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 3471 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.9%;
Best Local Similarity 68.6%;
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-715-568A-2
                                                                                                                                                                                                                                                                                                                                                                              US-08-747-121-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                               Mouse Polyimmunoglobulin Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 3095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.6%; Score 25.2; DB 5; Length 3 Best Local Similarity 71.7%; Pred. No. 20; Matches 33; Conservative 0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-968-751-3/C

Sequence 3.3 Application US/08968751

Sequence 3. Application US/08968751

Sequence 3. Application US/08968751

Sequence 3. Application US/08968751

APPLICANT: Rubinfeld, Bonnee

APPLICANT: Polakis, Paul G.

APPLICANT: Ligenfelter, Carol

APPLICANT: Ligenfelter, Carol

APPLICANT: Ungenfelter, Carol

APPLICANT: Wondy, Terliyn T.

TITLE OF INTENTION: MODULATORS OF BRCAI ACTIVITY

NUMBER OF SEQUENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCES: 0

CORRESPONDENCES: 0

STREET: 3031 Research Drive

CITY: Richmond

STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TITIAITITITITITIGGAATATAAAGCGGCCGCCATGGGCCCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 9480

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,751
FILNG DATE:
FILNG DATE:
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Glotta, Gregory
REGISTRATION NUMBER: 32.028
REGISTRATION NUMBER: ONYX1024 GG
TELEPHONE: (510) 222-9758
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3256 base pairs
TYPE: nucleic acid
PRIOR APPLICATION DATA: including a PRIOR APPLICATION DATA: described APPLICATION NUMBER: 08/367,395 FILING DATE: 12/30/94 ATONEY AGENT INFORMATION: NAME: 34,613 RESTRANCE/DOCKET NUMBER: 34,613 RESTRANCE/DOCKET NUMBER: 212/127 TELECOMMUNICATION INFORMATION: TELECHONE: (619) 552-8400 TELEFAX: (619) 552-8400 TELEFAX: 67-3510 TELEX: SEQUENCE LISTING TELEX: SEQUENCE LISTING INFORMATION FOR SEQ. ID NO: 7: SECUENCE CHARACTERISTICS: LENGTH: 3095 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                Coding Sequence 85....2400
                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
TOPOLOGY: DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: US
ZIP: 94806
                                                                                                                                                                                                                                                                                                                                                                                                                                            , NAME/KEY:
;
LOCATION:
US-08-434-000A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                 COUNTRY: USA

ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IDM PC COMPATIBLE
OPERATING SYSTEM:
OFFRAFING SYSTEM:
OFFRAFE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
ATONENT APPLICATION DATA:
APPLICATION NUMBER: US/07/750,080A
FILING DATE: 19910826
CLASSIFICATION: 435
ATONEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/106 IMMU
TELEPHONE: (703)836-9300
TELEFRX: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
33.6%; Score 25.2; D.
Best Local Similarity 90.0%; Pred. No. 6.1;
Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: 3.5" DISKETTE, 1.44 MD
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PETFECT 5.1
CURRENT: APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
                   ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 TITTATITITITITIGGAATATAAAGCG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 TTTTTTTTTTTTTTTGGCATATAAATCG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE: CLONE: P-artF(12) US-07-750-080A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703)663-4109
TELETAX: 899149
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: $1091e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ò

```
US-08-306-51B-16/C

105-08-306-51B-16/C

Sequence 16, Application US/08306691B

Patent No. 5734039

BAPLICANT: Calabretta, Bruno

APPLICANT: Calabretta, Bruno

APPLICANT: SADIABRES

TITLE OF INVENTION: OLIGONUCLEGITIDES TARGETING COOPERATING ONCOGENES

NUMBER OF SEGUENCES: SADIABRESS:

ADDRESSEE: SAGIABL ADDRESS:

ADDRESSEE: Two PADRESS:

ADDRESSEE: Pennsylvania

COMPUTEY: Philadelphia

COMPUTEY: Philadelphia

COMPUTER: Pennsylvania

COMPUTER: Pennsylvania

COMPUTER: BRABALE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 kb

COMPUTER: September 15, 1994

FILING DATE: SEPTEMBER: B30.480

RESISTRATION NUMBER: B30.480

REPERPONE: CALABACTERISTICS:

LENGHY: LASSI DASSE PALICS

LENGHY: LASSI DASSE PALICS

LENGHY: LASSI DASSE PALICS

TELEPHONE: TRUBERS: Gobble
                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 2436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCCAAAAATTGAAATTTTATTTTTTTTTTGGAATATAAAGCGGCCGCCA 52
                                                                                                                                                                                                                               Query Match 33.3%; Score 25; DB 4; Length 3256; Best Local Similarity 84.8%; Pred. No. 24; Matches 28; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 33.1%; Score 24.8; DB 2; Length 2. Best Local Similarity 67.3%; Pred. No. 25; Matches 35; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                      ; NAME/KEY: CDS
; LOCATION: 34..2541
US-08-968-751-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY:
US-08-306-691B-16
                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                        ò
```

Search completed: May 29, 2000, 22:08:54 Job time: 38735 sec

```
May 30, 2000, 09:48:19; Search time 2276.24 Seconds (without alignments) 147.011 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCCAAAATTGAAATTTTA......GCCCGGCCGCCAACGGCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pending_Patents_NA:*

1: /cgni_6/ptodata/1/pna/USO6_COMB.seq:*

2: /cgni_6/ptodata/1/pna/USO6_COMB.seq:*

3: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

5: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

6: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

7: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

8: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

9: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

10: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

11: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

12: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

13: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

14: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

15: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

16: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

17: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

18: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

19: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

20: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

21: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

22: /cgni_6/ptodata/1/pna/USO8_COMB.seq:*

23: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

24: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

25: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

26: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

27: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

28: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

29: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*

20: /cgni_6/ptodata/1/pna/USO8_BCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgnl_6/ptodata/1/pna/US088D_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ptodata/1/pna/US089G_COMB.seq:*
/ptodata/1/pna/US089H_COMB.seq:*
/ptodata/1/pna/US0891_COMB.seq:*
/ptodata/1/pna/US090A_COMB.seq:*
/ptodata/1/pna/US090B_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5142629 seqs, 2230885800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                              US-08-935-377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                      OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                                                                                                           Run on:
```

```
48: Cgnl. Sprodata/I pha/NS032_ComB.seq:
46: Cgnl. Sprodata/I pha/NS032_ComB.seq:
47: Cgnl. Sprodata/I pha/NS032_ComB.seq:
48: Cgnl. Sprodata/I pha/NS032_ComB.seq:
48: Cgnl. Sprodata/I pha/NS032_ComB.seq:
48: Cgnl. Sprodata/I pha/NS032_ComB.seq:
48: Cgnl. Sprodata/I pha/NS033_ComB.seq:
48: Cgnl. Sprodata/I pha/NS033_ComB.seq:
50: Cgnl. Sprodata/I pha/NS030_ComB.seq:
50: Cgnl. Sprodata/I pha/NS003_ComB.seq:
50: Cgnl. Sprodata/I pha/NS6001_ComB.seq:
50: Cgnl. Sprodata/I pha/NS6001_ComB.seq:
60: Cgnl. Sprodata/I pha/NS6000_ComB.seq:
60: Cgnl. Sprodata/I pha/NS6000_ComB.seq:
60: Cgnl. Sprodata/I pha/NS6000_ComB.seq:
60: Cgnl. Sprodata/I pha/NS6000_ComB.seq:
60:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

esult Ouery No. Score Match Length DB ID Description	Sequence 3, Appli Sequence 25, Appl
ΩI	75 28 US-08-935-377-3 59 28 US-08-935-377-25
DB	78 78 78
Query Match Length DB	75
Query Match	75 100.0 59 78.7
sult No. Score	75 59
Result No.	77

```
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 75; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GCCGCCAACGGCGGA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGCCAACGGCGGA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE:
US-08-935-377-25
                                                                                                                                                                                                                                                                                                                                                                                                                           , NAME/KEY:
; LOCATION:
US-08-935-377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                    Sequence 8, Appli
Sequence 10, Appli
Sequence 66, Appl
Sequence 66, Appl
Sequence 66, Appl
Sequence 72, Appl
Sequence 72, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 70, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 67, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 56, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 65, Appl
Sequence 11, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 111, Appl
Sequence 1111, Appl
Sequence 1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08935377

Sequence 3, Application US/08935377

GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: APC COMPATION

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin DATA:

APPLICATION NUMBER: US/08/935,377

FILING DATE: 22-SEP-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-196-362A-1517
US-08-196-362D-1517
US-09-401-665-4227
US-09-293-972-33060
VS-09-515-126-2413
VS-09-515-126-2413
US-09-353-690-1777
US-09-353-690-1777
US-09-351-4913
28 US-08-935-377-26
28 US-08-935-377-32
12 US-08-322-358-8
12 US-08-322-358-10
13 US-08-322-358-10
13 US-08-322-358-10
13 US-08-358-928-66
18 US-08-358-928-72
18 US-07-914-7388-77
19 US-08-358-928-70
18 US-08-358-928-70
18 US-08-358-928-70
18 US-08-358-928-70
18 US-08-358-928-70
18 US-08-358-928-70
19 US-08-558-928-67
11 US-08-558-928-67
12 US-08-358-928-67
13 US-08-358-928-65
14 US-08-358-928-65
15 US-08-358-928-65
18 US-08-358-928-65
19 US-08-358-928-65
10 US-08-358-928-65
             59

644723

647723

647723

65557444723

6557372

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6572

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772

6772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-935-377-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30.6
30.6
30.6
30.4
4.0
30.4
                                                                                                                                                                           00000
```

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-08-935-377-25
US-08-935-377-25
Sequence 25, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Vaccines Based Thereon
TITLE OF INVENTION: Vaccines Based Thereon
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Sterne Kessler, Goldstein & Fox P.L.L.C
STRET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: D. C.
COUNTER: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDION TYPE: Ploppy disk
COMPUTER: Eloppy disk
COMPUTER: Law PC Compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/935,377
CLASSIFICANION: 422-4
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Elic R
RESISTANTON NUMBER: 36,688
RESISTANTON NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELEPHONE: (202) 371-2600
TELEPHONE: COLOS 371-2600
INFORMATION FOR SEQUENCES
CHARACTERISTICS:
CERCENTER COLOS 371-2600
INFORMATION FOR SEQUENCES
CHARACTERISTICS:
CHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
NAME: Steffe, Eric K
REGISTRATION NUMBER: 16,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
REFERENCATION INFORMATION:
TELEPHONE: (202) 371-2500
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS:
LENGTH: 75 base pairs
LENGTH: 75 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 75; DB 28;
; Pred. No. 5.3e-09;
0; Mismatches 0;
```

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                ö
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GGCCAAAAATTGAAATTTTATTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCC 59
                                                                                                                      1 GGCCAAAAATTGAAATTTTATTTTTTTTTGGAATATAAAAGGGGCCGCCATGGGCCC 59
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                               Sequence 26, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF EQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STRIE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 78.7%; Score 59; DB 28; Length 59; Best Local Similarity 100.0%; Pred. No. 3.3e-05; Matches 59; Conservative 0; Mismatches 0; Indels
  Length 59;
Query Match 78.7%; Score 59; DB 28; Length 59 Best Local Similarity 100.0%; Pred. No. 3.3e-05; Matches 59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, N.W., Suite 600 STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377

FILING DATE: 22-SEP-1997

CLASSIFICATION: 424

ATTORNEY/AGBNT INFORMATION:
NAME: Steffe, Eric K

REGISTRATION NUMBER: 36,688

REFRENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 59 base pairs
TYPE: nucleic acid
STRANDEDWESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA
US-08-935-377-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                             RESULT 3
US-08-935-377-26/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-935-377-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                              å
                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
APPLICANT: FALKNER, Falko-Gunter
APPLICANT: BODEMER, Walter
APPLICANT: BODEMER, Friedrich
APPLICANT: MOSS, Bernard
ITTLE OF INVENTION: MATERIALS USING RECOMBINANT AVIPOX VIRUS VECTORS
INVERSEPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Alexandria SITREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria SITREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria SITAE: VA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,358
FILING DATE:
FILING DATE:
CLASSIFICATION NUMBER: US/08/322,358
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
CLASSIFICATION NUMBER: US/08/322,358
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/08/322,358
CALIF. 2000

CALIF. 2000

MEDIUM TYPE: Floppy disk

COMPUTER: Eloppy disk

COMPUTER: Eloppy disk

COMPUTER: Elba PC Compatible

COPERATIOS SYSTEM: PC-005/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,377

FILING DATE: 22-SEP-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K

REGISTRATION NUMBER: 1821.0010000/EKS/CMB

REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB

TELEPHONE: (202) 371-2500

TELEPHONE: (202) 371-250

TROCHH: 77 base pairs

TYPE: NUCLE: Calid

STRANDENESS: Single

TYPE: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGCCAAAAATTGAAATTTTTTTTTTTTTGGAATATAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42.4; DB Pred. No. 0.31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ION NUMBER: 29,768
/DOCKET NUMBER: 30357/108 KIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
APPLICATION NUMBER: US 07/734,741
FILING DATE: 23.JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30357/108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-322-358-8; Sequence 8, Application US/08323358; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: CDNA
US-08-935-377-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
```

```
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: V?
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
US-08-322-358-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                               δ
                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-372-358-9/C
US-08-322-358-9/C
US-08-322-358-9/C
Sequence 9, Application US/08322358
Sequence 9, Application
GENERAL INFORMATION:
APPLICANT: BODEMER, Walter
APPLICANT: DONNER, Friedrich
APPLICANT: MOSS, Bernard
TITLE OF INVENTION: PRODUCTION OF ISOLATED PROTEINACEOUS
TITLE OF INVENTION: MATERIALS USING RECOMBINANT AVIPOX VIRUS VECTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                              3 CCAAAAAITGAAATTITATTITTTTTTGGAATAIAAAGCGGCCGCCAIGGGCC 58
                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                              Score 40; DB 12; Length 84; Pred. No. 1.2; 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 22313-0229
COMPUTER READABLE FORM:
MEDIUM TYER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/322,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30357/108 KIST
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/882,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: APPLICATION NUMBER: US 07/734,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
IMMEDIATE SOURCE:
CLONE: Oligonucleotide oselP2
                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE: CLONE: Oligonucleotide oselP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (703)000
TELEX: 899149
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 86 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                     Query Match 53.3%;
Best Local Similarity 82.1%;
Matches 46; Conservative
                 (703)836-9300
(703)683-4109
                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                   TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                            CLONE: C
US-08-322-358-8
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

```
ö
                                                                                                                                                                                                             Sequence 10, Application US/08322358

Sequence 10, Application US/08322358

GRERAL INFORMATION:
GREEAL INFORMATION:
GREEAL INFORMATION:
GREEAL INFORMATION:
APPLICANT:
BONDER, Walter
APPLICANT:
BONDER, Friedrich
APPLICANT:
MOSS, Bernard
APPLICANT:
APPLICANT:
MATERIALS USING RECOMBINANT AVIPOX VIRUS VECTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Largher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CCAAAAATTGAAATTTTTTTTTTTTTTTGGAATATAAAGGGGCCGCCATGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 12; Length 4723;
Pred. No. 2.3;
0; Mismatches 10; Indels
DB 12; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 22313-029
ZIP: 22313-029
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,358
                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 30357/108 KIST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) IMMEDIATE SOURCE: CLONE: Plasmid pTKgpt-selp (4723bp) US-08-322-358-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/882,768
FILING DATE:
APPLICATION NUMBER: US 07/734,741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53.3%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 899149
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 4723 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
      53.3%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match , 53.3
Best Local Similarity 82.1
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (703)683-4109
      Query Match 53.3
Best Local Similarity 82.1
Matches 46; Conservative
```

```
Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
                                     Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                       3000 K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-651-472-66/c
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SCHEFFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: FALKNER, Falko Gunter
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFCIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 6474;
                                                                                            APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
APPLICANT: FALKNER, F. G.
APPLICANT: PFLEIDERER, M.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: EUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 19920720
CLASSITCATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: 0S 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/106 IMMU
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39.6; Di
Pred. No. 3;
0; Mismatches
                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                   STATE: VA
COUNTRY: USA
2.1P: -23313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIAL
OPERATING SYSTEM: PC-DOS/MS-DOS
                US-07-914-738B-66/c
; Sequence 66, Application US/07914738B
; GENERAL INFORMATION:
APPLICANT: DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-08-358-928-66/c
; Sequence 66, Application US/08358928
; GENERAL INFORMATION:
APPLICANT: DORNER, Friedrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149'
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 6474 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 83.33
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , CLONE: pselP-gp160MN
US-07-914-738B-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
APPLICANT: DORDER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: PALKNER, Falko Gunter
APPLICANT: PALKDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNOBEFCIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
CORRESPONDENCE: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3964 AAAAATTGAAATTTTATTTTTTTTTTTGGAATATAAAGGCCTCCATGGCC 3911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AAAAATTGAAATTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 6474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                          SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,768
PR: 30472/166/IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner STREET: 3000'K_Street, N.W., Suite 500
Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 39.6;
Pred. No. 3;
                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFENCE/DOCKET NUMBER: 30472/166/1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION (202)672-5300
                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 66, Application US/08651472 GENERAL INFORMATION:
                                                 COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DK
SOFTWARE: PatentIn Release #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20007-51199
COMPUTER READABLE FORM:
MEDIUM TYPE: 710PPy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.8%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202)672-5399
TELEX: 904135
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERICS:
LENGTH: 6474 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-358-928-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
```

```
Sequence 72, Application US/08358928
Sequence 72, Application
Sequence 72, Application
APPLICANT: SCHEIFLINGER: Friedrich
APPLICANT: SCHEIFLINGER: Falk Gunter
APPLICANT: FALKNER, Falk Gunter
APPLICANT: FILEIDERER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMBRIC
TITLE OF INVENTION: URBSES CONTAINING HUMAN IMMUNOBERCIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CCAAAAATTGAAATTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.8; DB 3; Length 5532;
Pred. No. 4.6;
0; Mismatches 12; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: USA

ZIP: 20007-5109

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358,928
FILING DATE:
                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REERERNCE/DOCKET NUMBER: 30472/106 IMMU
TELECOMMULICATION INFORMATION:
TELEPAX: (703)836-9300
TELEFAX: (703)83-4109
TELEFAX: (703)83-4109
TELEFAX: 899149
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 5532 base pairs
LENGTH: 6532 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TYPE: 11near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 79.3%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (202)672-5399
                                                                                                                                                                                                                                                                                                                                                        CLONE: pN2gpta-FIX
US-07-914-738B-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
US-08-358-928-72/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALENDER, F. G.
APPLICANT: PLEIDERER, M.
TITLE OF INVENTION: BURRAYOTIC CYTOPLASMIC DNA VIRUS GENOME
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 AAAAATIGAAATITITITITITITITIGGAATATAAAGCGGCCGCCAIGGGCC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,738B
FILING DATE: 19920720
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18;
                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
                                                                                                                         FILING DATA:

FILLING DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 07/914,738

FILLING DATE: 20-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/750,080

FILLING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BERNY. Stephen A.

REGISTRATION NUMBER: 39,768

REFERENCE/DOCKET NUMBER: 39,768

REFERENCE/DOCKET NUMBER: 30472/166/IMMU

TELEPHONE: (202)672-5399

TELEFAX: 904136

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 6474 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.6; DB; Pred. No. 3; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-07-914-738B-72/C
; Sequence 72, Application US/07914738B
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 52.8%;
Best Local Similarity 83.3%;
Matches 45; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-651-472-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22313-0299
                                                                                                                  FILING DATE:
```

ŏ

Gaps

ö

```
RESULT 14

US-07-914-73BB-70

Sequence 70, Application US/0791473BB
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED
TITLE OF INVENTION: BUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME
NUMBER OF SEQUENCES: 84
CORRESPONDENCES: 84
CORRESPONDENCE ADDRESS:
STREET: 180°C Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PARENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/914,738B
FILING DATE: 19927700
CLASSIFICATION 19435
CONTON AND TOWN 1435
                                                                                                                                                                                        3 CCAAAAATTGAAATTTTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCG
                                                                                                   Score 38.8; DB 18; Length 5532;
Pred. No. 4.6;
0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38.4; DB 3;
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDMESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/106 ITELECOMMUNICATION INFORMATION:
                                                                                                      51.78;
79.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.2%;
97.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                      Query Match 51.77
Best Local Similarity 79.37
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 97.5
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; CLONE: selP promoter US-07-914-738B-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
TELEX: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-358-928-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                g
                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-651-472-72/c
Sequence 72, Application US/08651472
APPLICANT: SCHEIFLINGER, Fitedrich APPLICANT: FALKNER, Fatedrich APPLICANT: FALKNER, Michael TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNOBEFCIENCY VIRUS TYPE 1 TITLE OF INVENTION: (HTV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 5532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER: ELABALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELAPORTIBLE
COMPUTER: PROPENTIBLE
COMPUTER: PAPE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
FILING DATE:
LENGTH: 5532 base pairs

TYPE: nucleic acid

STRANDEDRESS: single

TOPOLOGY: linear

MOLECULE TYPE: Other nucleic acid;

DESCRIPTION: Synthetic DNA oligonucleotide

IMMEDIATE SOURCE:

CLONE: pN2gpta-FIX

US-08-358-928-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Synthetic DNA oligonucleotide
                                                                                                                                                                                                                                                                                              51.7%; Score 38.8; Dilarity 79.3%; Pred. No. 4.6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30472/166/IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEE: Foley & Lardner
F: 3000 K Street, N.W., Suite 500
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-ULL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202)6/2-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 72
SEQUENCE CHARACTERISTICS:
LENGTH: 5532 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & LA
STREET: 3000 K Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-651-472-72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 46; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                          g
G
                                                                                                                                                                                                                                                                                                                                                                                     ö
```

ö

Gaps

ö

Length 49;

```
GENERAL INCRAMICON.

GENERAL INCRAMICON.

APPLICANT: DORNER, Friedrich
APPLICANT: PILEDERER, Friedrich
APPLICANT: PILEDERER, MICHEL
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRESE CONTAINING HUMAN IMMUNOBEFCIENCY VIRUS TYPE I
TITLE OF INVENTION: VIRESE CONTAINING HUMAN IMMUNOBEFCIENCY VIRUS TYPE I
TITLE OF INVENTION: VIRESE CONTAINING HUMAN IMMUNOBEFCIENCY VIRUS TYPE: DIRECT MOLECULAR CONTAINING HUMAN IMMUNOBER OF SEQUENCES: 95
CONTROPER SEADINGS (Street, N.M., Suite 500
CITY: Washington
STREET: 3000 Street, N.M., Suite 500
CITY: Washington
CONFUTER: IEM PC compatible
COMPUTER READALE FORM:
MEDIUM TYPE: FIDEPY disk
CONFUTER: IEM PC compatible
CONFUTER: 20-010-1992
FILING DATE: 20-010-1992
FILING DATE: 20-010-1991
ATTORNEY AGENT INFORMATION:
NAME: BENT, SEEPHEN A.
APPLICATION NUMBER: 29, 768
RECEIRATION NUMBER: 29, 768
RECEIRATION NUMBER: 20-300
TELERAN: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%; Score 38.4; DB 13; Length 49; 97.5%; Pred. No. 2.6; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear: TOPOLOGY: linear: MOLECULE TYPE: Other nucleic acid; DESCRIPTION: Synthetic DNA oligonucleotide; IMMEDIATE SOURCE: SelP promoter US-08-358-928-70
Sequence 70, Application US/08358928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.55
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

Search completed: May 30, 2000, 09:48:27 Job time: 60177 sec

gb_est26:'
gb_est27:'
gb_est28:'
gb_est29:'

em_est21: em_est22: gb_est30:

em_est20

gb_est31: gb_est32: em_est23:

em_est25: em_est26:

Sequence:

Title:

Run on:

Searched:

em_est24:

gb_est34: gb_est35:

gb_est33

gb_est36;

```
997:
998:
1000:
1010:
102:
104:
106:
106:
108:
                                                                                                                                                                                                       May 29, 2000, 21:13:10 ; Search time 2192.43 Seconds (without alignments) 138.655 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                         US-08-935-377-3
75
1 GGCCAAAAATTGAAATTTTA......GCCCGGCCGCCAACGGCGGA 75
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4857316 seqs, 2026611650 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est17:*
gb_est18:*
gb_est19:*
gb_est20:*
gb_est21:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_estilo:..
em_es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est10:*
gb_est11:*
gb_est12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est13:*
gb_est14:*
gb_est15:*
gb_est16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est22:
gb_est23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_est1::
em_est2::
em_est4::
em_est6::
em_est6::
em_est8::
em_est8::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
```

Database :

gb_est37:* gb_est38:* em_est27:* em_est28:*

em_est30: gb_est39:

em_est29:

gb_est40:*
gb_est41:*
gb_est42:*
gb_est43:*
gb_est44:*
em_est31:*

jb_est47:* jb_gss1:*

b_gss2

em_gss1: em_gss2:

em_gss3

gb_est45: gb_est46:

em_est33 em_est34 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9b_gss12:*
9b_gss13:*
9b_gss14:*
9b_gss14:*
9b_gss15:*

em_gss8:* gb_gss11:* gb_gss10:* em_gss9:*

gb_gss8: gb_gss9:

em_gss7

em_gss10: em_gss11: em_gss12:

SUMMARIES

Determination o collaboration w http://www.edqp	library (Dros B d'Etude du Poly project grant. and Genevieve P PREJOBACII.	Locati 112 / .12 / press / plasm / db_xx / clone / clone	286 a 29 286 a 20 28 a 20 29 a 29 conservat:	SAAP       STTI	006	AW297017 UI-H-BWO-ajf-d IMAGE:2731457 AW297017 AW297017:1 GI		Unpublished (1 On Dec 20, 1999 Contact: Rober Tel: (301) 496 Email: Robert, The sequence of oligonuclectic strand cDNA an tail. CDNA Lik NGI-GAP CLORA	www-bio.llnl.gelennts were clements were SGC_rich#Low_CSGq primer: M POLYA=Tes.  e   1   1   1   1   1   1   1   1   1	/not
COMMENT		FEATURES	ORIGIN ORIGIN Query Match Batches 15 Matches 2	Qy 9 A; Db 960 R; Qy 69 C	: 900 dd	ACCESSION VERSION	REFERENCE AUTHORS TITLE	JOURNAL	FEATURES SOUFCE	
Description	AL106303 Drosophil AW297017 UI-H-BW0- AL096911 Drosophil AQ74767 HS_5501_A	ALS/USDS UNIVAGOS.A. AQ755434 HS_5566_B A1964281 EST269395 AW297722 UI-H-BW0- AA33067 EST44123 A1902252 QV-BT003- AL069994 Drosophil AW026618 WV45c10.x	AA12344 mp94a05.r A1683617 tw52g505.x W30577 mc28a08.fl AW125685 UT-M-BH2. AW155524 mg1e0030P AQ782146 HS_3174_B AL05826 FRSOSOPHII	AU07390 AU07350 AL285735 qu81d09.x AL097859 Drosophil AL106206 Drosophil AW68602 x130f01.x AL253335 ap42all.x AL257634 aq92404.x	A0780818 HS_3104_B AL107369 Drosophil A1783861 tr29c08 x A178854 tr29c02 x	AA55039 0181C08.s AA660391 00266 WtR AL050448 Drosophil AL061241 Drosophil A167321 tu73b11.x A1633105 qz49904.x A1633105 qz49904.x	B20040 T782-T/-1 ALO74548 Drosephil AW074018 xb06d08.x AL45994 132209.x AA773220 af78e04.r AL629893 486041F08 AA947860 ox21901.s AQ320590 RPCIII-96	ALIGNMENTS  DNA  GSS  26-JUL-1999  er genome survey sequence 17 end of BAC 11brary from Drosophila melanogaster (fruit sequence.	racheata; Hexapoda; Insecta; a; Diptera; Brachycera; ilidae; Drosophila.	(E-mail : segret@genoscope.cns.rr
Query e Match Length DB ID	47.2 1201 83 44.5 158 79 40.8 1101 82 40.5 909 85	40.0 607 39.7 1404 39.2 468 38.9 230 38.9 644 38.9 1024	38.4 423 53 38.4 423 53 38.4 425 26 38.4 465 69 38.4 853 70 38.4 1062 82	38.1 194 38.1 372 38.1 953 37.9 261 37.9 421	37.9 409 44 37.9 710 90 37.9 1101 83 37.6 184 60 37.6 409 54	37.6 498 34 37.6 720 36 37.6 1101 82 37.6 1101 82 37.3 335 53 37.3 648 52	37.3 847 84 37.3 1101 82 37.1 224 64 37.1 248 46 37.1 389 38 37.1 522 52 37.1 602 105	01 bp nogast osbac urvey	AL106303. AL106303.1 GI:5621247 AL106303.1 GI:5621247 fruit fly. fruit fly. Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Bukaryota; Meoptera; Endopterygota; Diptera; Brachycera; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; I (bases 1 to 1201) Genoscope. Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequer	BP 191 91006 EVRY cedex - FRANCE - Web : www.genoscope.cns.fr)
Result No. Score	0 1 33.4 2 3 33.4 4 30.66		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			0	38 28 39 28 41 27.8 c 42 27.8 44 27.8 44 27.8 45 27.8 45 27.8	RESULT 1 CNS01651/C LOCUS DEFINITION	ACCESSION VERSION VERSION VERWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	

```
Jeus Metazoa; Chordata; Craniata; Vertebrata; Mammalia; primates; Catarrhini; Hominidae; Homo.

1 to 158)

http://www.ncbi.nlm.nih.gov/ncicgap.
Cancer Institute, Cancer Genome Anatomy Project (CGAP),
le Index
led (1997)

1) 1955 this sequence version replaced gi:1133426.
Robert Strausberg, Ph.D.
Robert Strausbergenh.gov
ncc contained an oligo-dr track that was present in the section that was used to prime the synthesis of first leotide that was used to prime the synthesis of first leotide that was used to prime the synthesis of first leotide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first locatide that was used to prime the synthesis of first location distribution information can be found through the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parism="Homo sapiens"
__xref="taxon:9606"
__xref="taxon:9606"
cone="inage:2731457"
lone_lib="NOL_GAP_Sub6"
lone_lib="NOL_GAP_Sub6"
bb_host="hulbB (life Technologies)"
ste="Vector: p1713D-Pac (Pharmacia) with a modified ...
      ro .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
of this BAC-end sequence was carried out as part of a with the European Drosophila Genome Project (EDGP) - up.ebi.ac.uk -. This Drosophila melanogaster BAC BAC) was made by Alain Billaud at CEPH (Centre Lymorphisme Humain) with funding provided by a MRC . The DNA was prepared from embryos by Alain Bucheton Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               onsortium/LLNL at:
.gov/bbrp/image/image.html The following repetitive e found in this cDNA sequence: 99-142,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 bp mRNA EST 16-JAN-2000 d.d-09-0-UI.sl NCI_CGAP_Sub6 Homo sapiens cDNA clone 37, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||:::::: |:| |||| | ::|::|||:| |::||::||::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITITITIGGAATATAAAGCGGCCGCCATGGGCCCGGCCGCCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                ation/Qualifiers
.1201
.1201
.ganism="Drosophila melanogaster"
lashid="pBeloBAC11"
__xref="taxon:7227"
lone_lib="DrosBAC"
.one="BACN15M07"
.ote="and:rf7"
.teg 283 t 150 oti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.2%; Score 35.4; DB 83;
47.5%; Pred. No. 7.8;
tive 22; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ation/Qualifiers
.158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _complexity
M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I:6703653
                    Determination
                              COMMENT
```

```
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 7e1: (206) 616-3887 Fax: (206) 616-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 909)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 153~{
m c} 34 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ743767 909 bp DNA GSS 16-JUL-1999 HS_5501_A1_C11_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic_clone Plate=1077 Col=21 Row=E, genomic_survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     2 GCCAAAAATTGAAATTTTATTTTTTTTTTGGAATATAAAAGCGGCCGCCATGGGCCCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                    Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. 909
/organism="Homo sapiens"
/orsanism="taxon:9606"
/clone="Plate=1077 Col=21 Row=E"
/clone_11b="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                             others
                                                                                                                                                                                                                                                                                                                    Query Match 40.8%; Score 30.6; DB 82; Length Best Local Similarity 49.2%; Pred. No. 1.2e+02; Matches 32; Conservative 17; Mismatches 16; Indels
                                                    1. 1101
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_rre="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN01A18"
                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                             H
                                                                                                                                                                                                                             330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 909.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              315 g
                                  Location/Qualifiers
                                                                                                                                                                                                                          175 g
                                                                                                                                                                                                    /note="end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ743767.1 GI:5521289
                                                                                                                                                                                                                          179 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
         pBeloBAC11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                940 TTGMC 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CCGCC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AQ743767
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNSOOYWS 1101 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACNO1A18 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Facilitate Gene Discovery. Genome Research 6, 791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neopiera; Endopierygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TITIATITITITITITGGAATATAAAGCGGCCGCCATGGGCCCGGCCGCCAACGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 79; Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.5%; Score 33.4; DB
72.9%; Pred. No. 49;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAG_LIB=NCI_CGAP-Lu13
TAG_TISSUE=lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_SEQ-GCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL096911.1 GI:5608522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 72.9
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNS00YW5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
```

ò g

Indels

Pred. No. 2.1e+02; 0; Mismatches 20;

```
Similarity 67.7%;
42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       255
                                                                                                                                                     108 GC 109
                                                                                                                  71 GC 72
     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
AI964281/C
                                                                                                                                                                                                      RESULT 6
AQ752434/c
LOCUS
                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
       Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                       à
                                                                                                                                                     셤
                                                                                      음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONSTITUTION ARRAYED by: Greg Lennon, Ph.D.

CONSTITUTION ARRAYED UNIVERSITY GENOME Sequencing Center

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
CGAP/PARGAP), Tumor Gene Index
Unpublished (1998)
On Mar 10, 1998 this sequence version replaced gi:2949517.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                         ö
                                                                                                                                                                                                                                                                                          AIS7055 607 bp mRNA EST 14-APR-1999 tm/9a09.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2164216 :similar to WP:Y57G11C.13 CE14950 ADP-RIBOSYLATION FACTOR ;, mRNA
                                                                                                                                          Gaps
                                                                                                         3 CCAAAAATTGAAATTTTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo saplens
Eukaryota, Matazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 607)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert Length: 1231 Std Error: 0.00
Seq primer: -400p from Gibco
High quality sequence stop: 441.
Location/Qualifiers

ce /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2164216"
/clone="IMAGE:2164216"
/tissue_type="anaplastic oligodendroglioma"
/lab_nost="DH10B"
                                                                           ö
                                          Length 909;
                                                                             Indels
                                           Score 30.4; DB 85;
Pred. No. 1.5e+02;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                  A1570555
A1570555.1 GI:4533929
EST.
                                             Query Match
Best Local Similarity 63.9%;
Matches 46; Conservative
                                                                                                                                                                                                                217 cccceeeeeee 228
                                                                                                                                                                                 63 CGCCAACGGCGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                     ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                     RESULT SAI570555
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                    임
                                                                                                                                                       윤
                                                                                                                                                                                        ð
                                                                                                                       ö
```

40.0%; Score 30; DB 48; Length 607;

Query Match

```
On Feb 19, 1999 this sequence version replaced gi:4145341.
On Feb 19, 1999 this sequence version replaced gi:4145341.
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Rashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3868
Fax: (206) 616-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 872)
Mahalras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Mahalras, G.G., Wallace, J.C., Smith, K., Svartzell, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/do.xxef="texon:9606"
/do.xxef="texon:9606"
/clone="plate=1142 Col=16 Row=J"
/clone=1ib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBACe3.6; Genomic sequence of BAC ends"
a 212 c 154 g 237 t 14 others
                                                                                                                                                                                                                                                                                                                                                                                            AC/52434 872 bp DNA GSS 19-JUL-1999 HS_5566_B2_E08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1142 Col=16 Row=J, genomic survey sequence-AQ752434 AQ752434.1 GI:5539592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                     11 TGAAATITTATTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCGGCCGCCAACG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AAAAATTGAAATTTTTTTTTTTTTTGGAATATAAAGCGGCCGC 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30; DB 90;
Pred. No. 1.9e+02;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class: BAC ends
High quality sequence stop: 872.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%;
ilarity 78.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ass: BAC ends
```

```
92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GCCGCCAACGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    102 GCCTCCTGTGG
                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA339067/c
                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
વૃવ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         á
                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Rasborinae; Danio.

E (pases 1 to 1404)

G Quackenbush, J., Lee, N., Tomb, J.-F. and Ekker, S. Generation of Esys from zebrafish

Unpublished (1999)

On May 18, 1998 this sequence version replaced gi:3136813.

Other ESTs: TC1242

Contact: John Quackenbush

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 3528

Fax: 301 838 0208

Email: johnq@tigr.org

3 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /close_lib="zebrafish, Steve Ekker"
/tissue_type="whole body"
/desue_type="whole body"
/dev_stage="maternal"
/lab_host="xil-Blue MRF,"
/lab_host="vector: pAD-GAL4; Site_l: EcoR1; Site_2: Xhol; This
/note="vector: pAD-GAL4. Site_l: EcoR1; Site_2: Xhol; This
library was constructed by directed cloning into the
EcoR1. Xhol sites of pAD-GAL4. Estimated Average insert size
approximately 1.2kb based on 15 clones, estimated titer
approximately 1.2kb based on 15 clones, estimated titer
approximately 1.2kb based on 15 clones, estimated titer
approximately 1.2kb for a 12 chers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 468)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tational Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1134505.
AI964281 1404 bp mRNA EST 20-AUG-1999 EST269395 zebrafish, Steve Ekker Danio rerio cDNA clone RZBDA89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW297722 468 bp mRNA EST 16-JAN-2000 UI-H-BW0-ajh-h-05-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone IMAGE:2732001 3', mRNA sequence. AW297722 GI:6704358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CCAAAAATTGAAATTTTTTTTTTTTTTTTGGAATAAAAGCGGCCGCCATGGGCCCGGC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.7%; Score 29.8; DB 63; Length 1404; Best Local Similarity 66.2%; Pred. No. 1.8e+02; Matches 43; Conservative 0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="RZBDA89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1404
                                                                                        AI964281.1 GI:5756994
                                                mRNA sequence.
AI964281
                                                                                                                                                                Danio rerio
                                                                                                                                      zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1291 CCCCA 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 CGCCA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW297722/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                          DEFINITION
                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                     ACCESSION
                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
```

```
//doce=Nost=-Dritub (Life Technolagies)
//doce=Dritub (Life Technolagies)
//doce=Nost=-Dritub (Life Technolagies)
//doce=Dritub (Life Clonelagies)
//doce=Dritub (Life Technolagies)
//d
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Tel: (301) 496-1550
Email: Robert_Strausberg@hlh.gov
The sequence contained an oligo-dr track that was present in the oligouclectide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NGI-GGAP clone distribution information can be found through the L.M.A.G.E. Consortium/Lib.a.:
Www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 15-66, >MLTIE#LTR/MalrR POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGCCAAAAATTGAAATTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NCI_CGAP_Sub6"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 29.4; DB 79;
Pred. No. 3.2e+02;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism-"Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:2732001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAG_LIB=NCI_CGAP-Lu13
TAG_TISSUE=lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.2%;
Best Local Similarity 63.4%;
Matches 45; Conservative (
```

```
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-"organ: Dreast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived if on OrBESTES POR (U.S. Letters Patent application No 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mink and cDNA amplification were performed under low ming and cDNA amplification were performed under low at 112 c 116 g 256 t 19 others
                                                                                                                                                                                                                                                                                                                                                                                                      Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=QV&t2=QV-BT003-029.html&t3=04119&&t4=1)
Seq primer: puc 18 forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR30J05 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                      Eucharyote...

Eutheria: Perimates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 644)

HGP http://www.ludwig.org.br/ORESTES.

HGP http://www.ludwig.org.br/ORESTES.

On Dec 20, 1995 this sequence version replaced gi:1124918.

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GGCCAAAAATTTTTTTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
38.9%; Score 29.2; DB 62
Best Local Similarity 62.2%; Pred. No. 3.2e+02;
Matches 46; Conservative 0; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT003"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL069994.1 GI:4950125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 GGGGGGGGGGGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCCGCCAACGGCGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNSOOF3L
                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                    Legas, finance, finan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression
Le IIGR Human Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1902252 644 bp mRNA EST 01-DEC-1999 QV-BT003-041198-029 BT003 Homo sapiens CDNA, mRNA sequence. A1902252 A1902252.1 GI:6492730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
      AA339067 230 bp mRNA EST 21-APR-1997 EST44123 Fetal brain I Homo sapiens cDNA 5' end similar to EST containing Alu repeat, mRNA sequence.
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 12, 1996 this sequence version replaced gi:1393066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 38.9%; Score 29.2; DB 32; Length 230; Best Local Similarity 81.0%; Pred. No. 4.7e+02; Matches 34; Conservative 0; Mismatches 8; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Kerlavage, AR Bioinformatics Research The Institute for Genomic Research The Addical Center Drive, Rockville, MD 20850 USA Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            For clone availability, additional sequence and ex For clone availability, additional sequence and ex information related to this EST, please check the infex (http://www.tigr.org/tdb/hgi/hgi.html) seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCCAAAAATTGAAATTTTTTTTTTTTTGGAATATAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="ATCC (inhost):140684"
/db_xref="taxon:9606"
/clone_lib="Fetal brain I"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
                                                                                                             AA339067.1 GI:1991315
                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
A1902252/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                         DEFINITION
                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
```

g ò

Gaps

COMMENT

```
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia;
Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Mammalia;
Eutheria: Rodentia: Sciurognathi; Muridae: Murinae: Mus.

1. (bases 1 to 378)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Ten,F., Underwood,K., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:430248.
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 134 286 1800
Fax: 134 286 1810
Fax: 134 286 1800
                                                        AA123454 378 bp mRNA EST 17-FEB-1997 mp94a05.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:576848 5'. mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 AAACAAGGCTGTTTTTTTTTTTTTTTAAAAAAAAAGGTGGCCCTGCGGCCCCCCC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AAAAATTGAAATTTTATTTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCGGCCG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:576848"
/clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 38.7%; Score 29; DB 64; Best Local Similarity 63.8%; Pred. No. 4.4e+02; Matches 44; Conservative 0; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 367.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090" ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="male"
/tissue_type="Thymus"
/dev_stage="4 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA123454
AA123454.1 GI:1681489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 CCATAGGGG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 CCAACGGCG 73
                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
AA123454/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: n bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         wv45c10.x1 NCI_CGAP_Gas4 Homo saptens cDNA clone IMAGE:2532498 3's similar to gb:X06409 RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN AW02618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 rolate)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

On Jul 7, 1999 this sequence version replaced gi:5405757.

Contact: Robert Strausberg, Ph.D.

Email: Robert Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert Strausbergenih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GCCAAAAATTGAAATTTTATTTTTTTTTTGGAATATAAAGCGGCCGCCATGGGCCCCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xxef="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BaCR30J05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29.2; DB 82;
Pred. No. 2.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ww-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        189 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-"end : TET3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW026618
AW026618.1 GI:5880237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 38.9%;
Best Local Similarity 43.8%;
Matches 32; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       958 GSCCMRRGGGGGG 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 CCGCCAACGGCGG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260
```

LOCUS

RESULT 1 AW026618

쉽 ð ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

BASE COUNT ORIGIN

FEATURES

ô

Gaps

ö

```
Mulifact.

Seq primer:

High quality sequence stop: 423.

High quality sequence stop: 423.

Location/Qualiflers

1. 425

Corganism="Max musculus"

/ Ab_raf="taxon:1008"

/ Ab_host="1b="Soares mouse panMF19.5"

/ Ab_host="DH10B (ampicillin resistant)"

/ Ab_host="Pertor: pTT73D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA polylinker; Site_1: Not I; -01go(dT) primer [5]

/ Aparmacia Not I - 01go(dT) primer [5]

/ Aparmacia Not I - 01go(dT) primer [5]

/ Aparmacia Not I - 01go(dT) primer [6]

/ Aparmacia Not I - 01go(dT) primer [6]

/ Aparmacia Not I - 01go(dT) primer [7]

/ Aparmacia Not I - 01go(dT) primer [7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W30577 425 bp mRNA EST 11-SEP-1996 mC28a08.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone INAGE:349814 5' similar to gb:U08378 Mus musculus acute phase Hesponse factor (MOUSE);, mRNA sequence.
                                                                                                                                                               151 AAAAAGGGGAATITITITCCTITITITTGGGCCCCCAAAGGGGCCCCCGGGGGTTGGGGGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Mammalia;
                                                                                                               5 AAAAAITGAAAITITAITITITITITITGAAIATAAAGCGGCCGCCAIGGGCCCGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26; Length 425;
               Length 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                     Indels
                  Score 28.8; DB 53;
Pred. No. 4.7e+02;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.4%; Score 28.8;
                          38.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W30577.1 GI:1310546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 425)
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nouse mouse.
                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:221614
                                                                                                                                                                                                                               65 CCAA 68
                                                                                                                                                                                                                                                                                  GCTA 88
                             Query Match
Best Local Simi
Matches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                            RESULT 1:
W30577/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                             g
                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (base 1 to 433)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Tumor Gene Index

On May 18, 1998 this sequence version replaced gi:3138026.

Contact: Robert Strausberg@nlh.gov

Tal: (301) 496-1550

Email: Robert_Strausberg@nlh.gov

Email: Robert_Strausberg@nlh.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Praparation: Life Technologies, Inc.

CDNA Library Praparation: Life Technologies, Inc.

CDNA Library Praparation: Carga Cannon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

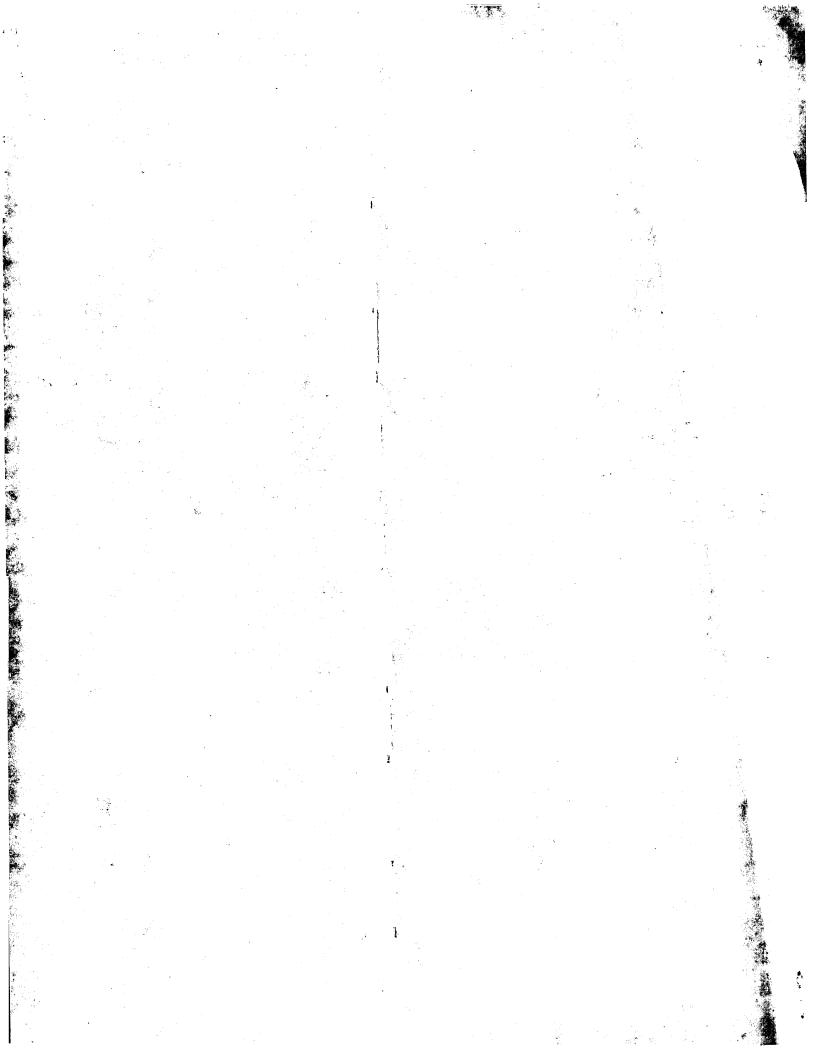
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINE at:
  /note-"Organ: uterus; Vector: pCNV-SPORTS; Site_1: Sall; /note_2: Not!; Cloned unidirectionally. Primer: Oligo dT. Site_2: Not!; Cloned unidirectionally. Primer of Step Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AIG83617 423 bp mRNA EST 15-DEC-1999 tw22905.x1 NCI_CGAP_Ut1 Homo sapiens cDNA clone IMAGE:2263352 3/ similar to contains element MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .423
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:2263352"
/clone=lib="NCI_CGAP_Utl"
/tissue_Lype="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                               Score 28.8; DB 28; Length 378;
Pred. No. 4.9e+02;
0; Mismatches 12; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 TIGAAAITITATITITITITIGGAAIAIAAAGCGGCCGCCAIGGGC 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insert Length: 1888 Std Error: 0.00 seq primer: -400P from Gibco High quality sequence stop: 417.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Б
/lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
A1683617
A1683617.1 GI:4893799
                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.4%;
Best Local Similarity 75.0%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11538-014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                  Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101
                                                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
AI683617/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
```

g δ

	0;
	Gaps
	; 0
14:	Indels
	+02; 12;
	Pred. No. 4.7e+02; ); Mismatches 12;
	l. No. Ismat
	Pred 0; M
	75.0%; ative
	1larity Conserva
	1 S1m. 36;
	Best Local Similarity 75.0%; Pred. No. 4.7e+02; Matches 36; Conservative 0; Mismatches 12

7		4	
ဂ္ဂ	_	Ω 4	
AAGCGGCCGCCATGG	= - ==	AAGAGGAACCICIGG	
TATA	=	TTA	
GGAA	=	TTAA	
10 IIGAAAITITATITITITITIGGAATATAAAGCGGCCGCCAIGGGC 57		91 TITAAITCITATITITITITITITAATITAAAGAGGAACCICTGGGC 44	
0 17	_	1	
, 1		σ.	
õ		검	

Search completed: May 29, 2000, 21:13:13 Job time: 36512 sec



7

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                            Length DB
                                      em_hum5:
gb_pl3:*
                                                                                                                                                                                                                                                                                                                           4768
4783
4887
4950
4967
                                                                                                                                                                                                                                                                                                                                                               55144
55187
55187
55187
55187
66187
66187
66187
793
338
338
340
144
                                                                                                                                                                                                                                                               4144
4267
4373
44443
4670
4670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2958
2958
2951
2961
                                                                                                                                                                    Query
Match
Score
                                                                                                                                                                                          70.8
69
                                                                                                                                                                                                                 \begin{matrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{matrix}
                                                                                                                                                                                                                                                         O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00000000000
                                                           (without alignments)
909.139 Million cell updates/sec
                                                                                          145
I GGCCAAAAATTGAAAAACTA......TTGTTTTTGTGGGCCCGGCC 145
                                                     May 29, 2000, 21:35:19 ; Search time 1214.87 Seconds
                                                                                                                                                     1765538
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                       882769 segs, 3808571567 residues
                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                     nucleic search, using sw model
                                                                                                                IDENTITY_NUC Gapox 1.0
                                                                                  US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                          gb_un:*
gb_v1:*
em_fun:*
em_hum1:*
em_hum2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_sy:*
em_un:*
em_vi:*
gb_htgl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_ba1:*
em_ba2:*
em_hum3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_htg3:*
gb_htg4:*
gb_htg5:*
                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_hum4:*
                                                                                                                                                                                                                                                                                                             gb_pr3:*
gb_ro:*
gb_sts:*
gb_sy:*
                                                                                                                                                                                                                                                                                                                                                                                               em_or:*
em_ov:*
em_pat:*
em_ph:*
em_ph:*
em_ph:*
em_pr:*
                                                                                                                                                                                                                                  9b_ba1:*
9b_om:*
9b_om:*
9b_ov:*
9b_pat:*
9b_p1:*
9b_p11:*
                                                                                                                                                                                                                                                                                                                                                                                        em_om: *
                                                                                                                                                                                                                          GenEmbl:*
                                                                                          score:
                                                                                                               Scoring table:
                                      OM nucleic
                                                                                                                                                                                                                           Database :
```

X5232 FBluescript
X5232 FBluescript
LO8784 Bluescript
LO8785 Bluescribe
LO8736 Veast integ
LO8735 Veast integ
LO8374 Cloning vec
LO8740 Yeast centr
LO8742 Yeast centr
LO8742 Yeast centr
LO8742 Yeast centr
LO8751 Cloning vec
LO8751 Cloning vec
LO8751 Cloning vec
LO8751 Cloning vec
LO8751 Yeast integ
LO8751 Yeast integ
LO8751 Yeast centr
LO8751 Yeast centr
LO8751 Yeast centr
LO8751 Yeast centr
LO8751 Cloning vec
LO8751 Yeast Centr

A44281 Sequence 9 X52326 pBluescript X52331 pBluescript AF072997 Cloning

A44281 ARBLKSM ARBLZKSP ARBLZKSP SYNBLKSPV SYNBLKSPV SYNBLKSPV SYNPBENGE XXU35131

AF072997

SUMMARIES

Searched:

Sequence:

Run on:

ALIGNMENTS

AF072538 CIONING V AF01571 Magnaport M22847 Cloning vec M22848 Cloning vec U82676 Aphelocoma

XXU25059 PRS305 CVU14125 PRS315 ASAJ5323 SYPPGR8V AR01477 AF01571 SYPPLKRB AF01571 SYPPLKRB AFU1577 AF01571 AF01577 AF0157 AF0157

X52324 PBluescript X52325 PBluescript X52330 PBluescript X52328 PBluescript L08787 BlueScribe L08786 BlueScribe L04797 Cloning vec

SYNBLDKPV SYNBLSKMV

```
1 (bases 1 to 259)
Analdey, A.C., Kun, M., Sharkey, A.M., Hargreave, T.B. and Cooke, H.J. AZOSPERY, A.C., Kun, M. D. TREATMENT
AZOSPERIA IDENTIFICATION AND TREATMENT
Patent: WO 9511300-A 9 27-APR-1995;
MEDICAL RES COUNTL (GB)
Other publication AU 7947794 950508.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (200-FEB-1990) Thomas B.A., Stratagene Clonin Systems, 11099 North Torney Pines Rd., La Jolla, CA 92037, USA C pases; 1 to 2958)
Short,J.W., Fernandez,J.W., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequence; cloning vector; expression vector; vector. synthetic construct. synthetic construct artificial sequence.

1 (bases 1 to 2958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARBLKSM 2958 bp DNA circular SYN 10-MAY-1995
pBluescript KS(-) vector DNA, phagemid excised from lambda ZAP.
X52326
X52326.1 GI:58064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB 14; Length 2958; Pred. No. 7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                   Length 259
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
47.6%; Score 69; DB 5; Length 259
Best Local Similarity 88.2%; Pred. No. 5.7e-12;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="phagemid pBluescript KS(-)"
754 c 731 g 765 t
                                                                                                                                                                                                                                                                     /db_xref="taxon:32644"
/clone_lib="MOUSE GENOMIC LIBRARY"
/clone="M3.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 2958
/organism="synthetic construct"
/db.xref="taxon:32630"
1. 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2958)
Alting-Mees,M.A. and Short,J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
                                                                                                                                                                                                                                                                                                                             69 t

    .259
    /organism="unidentified"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             63 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 GGGGCCTAACTAACTATTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 GGGGGCCCGGTACCCAGCTTTTGTT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.6%;
88.2%;
A44281.1 GI:2299115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submission
                                                 unidentified.
unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88319944
                                                                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
FEATURES
                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
 ACCESSION
                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
ARBLKSM
LOCUS
                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="aminoglycoside phosphotransferase"
/protein_id="amcoside phosphotransferase"
/db_xref="Gi:384002"
/translation="MIEQDGLHAGSPAMYERLFGYDWAQQTIGCSDAAVFRLSAGGR
/translation="MIEQDBARLSWIATTGVPCAVLDVYTEAGRDWLLLGEVPGQDL
LSSHLAPARKVSIMADARRELHTLDPATGFDHQARHRIBBARTRWEAGLVDQDLDE
ENGGLAPAELFARLKASMPDGEDLVVTHGDACLFNIMVENGFSGFIDGGRLGVADRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (22-JUN-1998) Technical Services, Stratagene, 11011 N.
Torrey Pines Rd., San Diego, CA 92037, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 GCAGAAACTCATCTGTGAAGAGGATCTGGCCCGGGCGGATCCCCCGGGCTGCAGGAATTC 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GAAAAACTAGATCTATTTATTGCACGCGGCCGCGGGATCCCCCGGGGTGCAGGAATTC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-MAR-1997
                                                                        02-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ODIALATRDIAEEGGEWADRELVLYGIAAPDSQRIAEYRLLDEEF"
3469. .4316
//note="Cole! origin of replication"
// 1116 c 1107 g 1047 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70.8; DB 14; Length 4326;
Pred. No. 1.9e-12;
0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                     1. ..4326
/organism="Cloning vector pcMVTAG3a"/db_nost="taxon:78249"
/lab_host="Escherichia coli K12"
1. .602
/note="CMV promoter"
/13. .799
/note="multiple cloning site"
859. .1242
/note="X940 polya signal region"
1242. .1703
/note="fl origin of replication"
1704. .1835
/note="Ppla promoter"
1836. .2227
/note="Sy40 origin of replication"
/note="Sy40 origin of replication"
/note="Sy40 origin of replication"
/note="Sy40 origin of replication"
                                                                    AF072997 4326 bp DNA circular SYN Cloning vector pCMVTAG3a, complete sequence. AF072997 GI:3284001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1228. .3022
function="kanamycin resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A44281 259 bp DNA
Sequence 9 from Patent W09511300.
                                                                                                                                                                Cloning vector pCMVTAG3a.
Cloning vector pCMVTAG3a
artificial sequence; vectors.
1 (bases 1 to 4326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 48.8%;
Best Local Similarity 76.3%;
                                                                                                                                                                                                                                                          pCMVTAG3a
Unpublished
2 (bases 1 to 4326)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A44281/c
LOCUS
DEFINITION
                                                                                       DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                               JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                     AUTHORS
                                      RESULT
AF072997
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
```

Gaps ö

7

```
cloning vector; expression vector; vector

    .2961
    /organism-"synthetic construct"

                                                                                                                                                                                                                                                                                    Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 GGGGCCTAACTAACTATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           747 GGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X52327.1 GI:58061
artificial sequence;
synthetic construct.
synthetic construct
artificial sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial sequence.
1 (bases 1 to 2961)
Thomas, E.A.
                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
FEATURES
                            ORGANISM
                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                         TITLE
JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARBL2KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90067967
4 (bases 1 to 2958)
Lampe,D.J., Grant,T.E. and Robertson,H.M.
Factors affecting transposition of the Himarl mariner transposon in
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (20-FFB-1990) Thomas E.A., Stratagene Clonin Systems,
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
2 (bases 1 to 2958)
Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacteriophage lambda expression vector with in vivo
                         ARBLKSP 2958 bp DNA circular SYN 11-JUN-1998
PBluescript KS(+) vector DNA, phagemid excised from lambda 2AP
X52331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cloning vector; expression vector; vector
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARBL2KSM 2961 bp DNA circular SYN 10-MAY-1995 pBluescript II KS(-) vector DNA, phagemid excised from lambda 2APII.
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.6%; Score 69; DB 14; Length 2958; Best Local Similarity 88.2%; Pred. No. 7e-12; Matches 75; Conservative 0; Mismatches 10; Indels
10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 2958
/note="phagemid pBluescript KS(+)"
/734 c 751 g 724 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .2958
/organism="synthetic construct"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 2958)
Alting-Mees,M.A. and Short,J.M.
Bluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics 149 (1), 179-187 (1998)
98250682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 GGGGCCTAACTAACTAATTTTGTT 130
                                                                                  106 GGGGCCTAACTAATTTTGTT 130
                                                                                                  747 GGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  artificial sequence; cl
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 2958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X52329
X52329.1 GI:58060
                                                                                                                                                                                                                           X52331.1 GI:58065
Conservative
                                                                                                                                                                                                                                                                                                                    Thomas, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                88319944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
ARBL2KSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                          RESULT
ARBLKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                     ద
                                                                                     ç
                                                                                                             g
```

```
synthetic construct.

Synthetic construct.

synthetic construct.

artificial sequence.

I (bases 1 to 2961)

S Thomas, E.A.

Direct Submission

L Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems, 11099 North Torney Pines Rd., La Jolla, CA 92037, USA

I (bases 1 to 2961)

I (canbda 2AP: a bacteriophage lambda expression vector with in vivo exclain properties

Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
2 (bases 1 to 2961)
Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacterlophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cloning vector; expression vector; vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARBL2KSF 2961 bp DNA circular SYN 10-MAY-1995
PBluescript II KS(+) vector DNA, phagemid excised from lambda
ZAPII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 47.6%; Score 69; DB 14; Length 2961; Best Local Similarity 88.2%; Pred. No. 7e-12; Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .2961
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .2961
/note="phagemid pBluescriptII KS(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                (bases 1 to 2961)
Alting-Wees, M.A. and Short, J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 2961)
Alting-Mees,M.A. and Short,J.M.
Palluscript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
```

ò g

δ g

```
KpnI-DraII-ApaI-XhoI-SalI-ClaI-HindIII-EcoRV-EcoRI-PstI-
SmaI-BamHI-SpeI-XbaI-NotI-XmaIII-BstXI-SacII-SacI SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GIGGAICCCCGGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACGGIGGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 GIGGAICCCCCGGGCIGCAGGAAITCGAIAICIAGCIIAICGAIACCGICGACCICGAGG 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obtained from VecBase 3.0
Unpublished (1991)
These data and their annotation were supplied to GenBank by Gilbert under the auspices of the GenBank Currator Program. BlueScribe KS Plus - Cloning vector #TYPE DNA CIRCULAR FILLE BlueScribe KS Plus - Cloning vector Paramar BlueScribe SS Plus - Cloning Paramar BlueScribe SS Plus - Cloning vector DATE 28-JAN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 14; Length 2964; Pred. No. 7e-12; 0; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #checksum 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                       start of T7-RNA synthesis 774 (c) start of T3-RNA synthesis 1976-2764 789-1 (c) Ap-R; b-lactamase POLYLINKER
                                                                                                                                                                                                                                                                              phage f1
) pucl9
T7 promoter
) BluekS-polylinker
                                                                                                                    17 promoter
) BlueKS-polylinker
) T3 promoter
puCl9c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYN
                                                                                                                                                                                                                                                                                                                                    653-760 108-1 (c) Biuers-poly1inke 772-791 20-1 (c) T3 promoter 755-1031 237-2964 2686-754 (c) pUC19 Conflict (cfl) and Mutations (mut): none
                                                                                                                                                                              795-2964 448-2617 pUC19c
Conflict (cfl) and Mutations (mut): none
VecBase(3):BlueKSp, VecBase(3):BlueSKm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/db_xref="taxon:32630"
756 c 735 g 765 t
                                                                          phage fl
puci9c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #resistance Ap
#Indicator beta-galactosidase
#indicator beta-galactosidase
SUMMARY BlueKSm #length 2964
Location/Qualifiers
1. .2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNBLKSPV 2964 bp DNA cir
BlueScribe KS Plus cloning vector
L08785
                                                                                                                                                                                                                                          Features of BlueKSm (2964 bp)
                                         Features of BlueKSm (2964 bp)
                                                                                                                                         00
                                                                                                                                                                                                                                                                            5488-5943
449- 285 (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGGCCTAACTAACTATTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747 GGGGGCCCGGTACCCAGCTTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic construct DNA.
synthetic construct
artificial sequence.
1 (bases 1 to 2964)
Gilbert, W.
                                                                                                                                                             20-
448-2617
                                                              source
5488-5943
236- 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.6%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L08785.1 GI:310729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ๙
                                                                                                                                                                                                                          PARENT
                        PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYNBLKSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lacZ region is on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #number 1
#authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic construct DNA.

synthetic construct
synthetic construct
1 (bases 1 to 2964)

Glibert, W.

Obtained from VocBase 3.0
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will Glibert under the auspices of the GenBank Currator Program.

BlueScribe KS Minus - Cloning vector
ENTRY BLUEKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #journal Gene (1987) in press fritation Sequence data from StrataGene facitation Sequence data from StrataGene CONMENT Sequence Correction according to Stratagene COMMENT Obtained from StrataGene on floppy disc.

Revised 02-FEB-1987 by F. Pfelffer:

14,09,10 'AT' to 'TA' to match revised sequence of PBR322

Revised 4-MAR-1987 to match sequence of pUC19 on request
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of Stratagene
Polylinker region revised 03-APR-1987 according to Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'vecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
VecSource(3):bGalKS, GenBank(50):PF1#brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This vector contains the fl origin so that the minus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                        26-JUL-1993
                                                                                                                                                                                      ó
                                                                                                                                             Query Match 47.6%; Score 69; DB 14; Length 2961;
Best Local Similarity 88.2%; Pred. No. 7e-12;
Matches 75; Conservative 0; Mismatches 10; Indels
                        7...2961
/note="phagemid pBluescriptii KS(+)"
/738 c 755 g 721 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                SYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE BlueScribe KS Minus - Cloning vector DATE 28-JAN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                circular
                                                                                                                                                                                                                                                                                                                                                                                                                                           INESCRIBE KS Minus cloning vector
          /db_xref="taxon:32630'
                                                                                                                                                                                                                                                                                                             106 GGGGCCTAACTAACTTTTGTT 130
                                                                                                                                                                                                                                                                                                                                              GGGGGCCCGGTACCCAGCTTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #sequence 02-FEB-1987
#sequence 04-MAR-1987
#sequence 03-APR-1987
ACCESSION VB0077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VecBase(3):BlueM13m
#parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L08784
L08784.1 GI:310728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNBLKSMV
                                                                      747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
ACCESSION
                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                    747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNBLKSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
```

ö

Gaps

ö

26-JUL-1993

ĺ

```
/transl_table=11
/product=aninoglycoside 3'-phosphotransferase"
/product=aninoglycoside 3'-phosphotransferase"
/product=aninoglycoside 3'-phosphotransferase"
/db_xref="G1:1345434"
/db_xref="G1:1345434"
/translation="MBHIORESCERPRINSNMDADLYGYKWARDNVGOSGATIYRLY
/kranslation="MBHIORESCERPRINSNMDADLYGYKWARDNVGOSGATIYRLY
/kranslation="MBHIORESCERPRINSNMDADLYGYKWARDNVGLATAIP
/gktargovleeyposganivDalavflrrisiprocopyrythgDeschonglycopyrythgDescerpscerpoord
/possponderinglycopyrythgDescerpscerpscerpoord
/possponderinglycopyrythgDescerpscerpscerpoord
/possponderinglycopyrythgDescentrations/
/possponderinglycopyryt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_1d="Baal2825.1"
/db_xref="G1:1345435"
/db_xref="G1:1345435"
/fb_xref="G1:1345435"
/fb_xref="G1:1345435"
/frenslation="MSIGHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY_IELDLNSGXILESFRPERFPMSFFKVILCGAVLSRIDAGOEQLGRRIHYSGNDLVE_XSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNPBEN66 ·3306 bp DNA circular SYN 06-FEB-1999 Cloning vector pBEN66 DNA for aminoglycoside 3'-phosphotransferase, beta-lactamase, complete cds.
                                                                                                                                                             46 GIGGAICCCCCGGGCTGCAGGAAITCGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                            /hote="derived from Tn903; kanamycin resistance gene"
/citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D85525.1 GI:1345433
D85525.1 GI:1345433
plasmid; aminoglycoside 3'-phosphotransferase; beta-lactamase.
Cloning vector pBEN66 (lab_host:E.coli) plasmid:pBEN66 DNA.
Cloning vector pBEN66
artificial sequence; vectors.
I (bases 1 to 3306)
Yamamoto, Y.
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (23-MAY-1996) to the DDBJ/EMBL/GenBank databases.
Yoshihiro Yamamoto, Hyogo College of Medicine, Department of
Genetics; Mukogawa-cho 1-1, Nishinomiya, Hyogo 663, Japan
(Tel:0798-45-6587, Fax:0798-40-7639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto,Y. and Furuyama,J.
One-step disruption by circular DNA in Escherichia coli
Unpublished (1996)
                                                                                     ô
    Length 2964;
47.6%; Score 69; DB 14; Length 29
88.2%; Pred. No. 7e-12;
ive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="amp"
/note="amipicillin resistance gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Cloning vector pbBN66"
/plasmid="pbBN66"
/db_xref="taxon:47800"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(2209. .3069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="T3 promoter"
                                                                                                                                                                                                                                                                                                                              106 GGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260. .1075
/gene="kan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260. .1075
/gene="kan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"amp
Query Match
Best Local Similarity 88.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNPBEN66/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                              d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lacZ region is on the complementary strand.
                                                                                                                                                                                                                                                                                        #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                                                                                                                                                                                                                            #journal Gene (1987) in press
#citation Sequence data from StrataGene
#comment sequence correction according to Stratagene COMMENT
Obtained from StrataGene on floppy disc.
Revised 02-FEB-1987 by F. Pfelffer:
1409/10 'AT' to 'TA' to match revised sequence of PBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of Stratagene Polylinker region revised 03-APR-1987 according to Stratagene COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KpnI-DraII-ApaI-XhoI-SalI-ClaI-HindIII-EcoRV-EcoRI-PstI-
SmaI-BamHI-SpeI-XbaI-NotI-XmaIII-BstXI-SacII-SacI SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
VecSource(3):bGalKS, GenBank(50):PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This vector contains the fi origin so that the plus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o43 start of T7-RNA synthesis 774 (c) start of T3-RNA synthesis 1976-2764 789-1 (c) Ap-R; b-lactamase POLYLINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #checksum 690.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 T7 promoter
20 1 (c) BlueKS-polylinker
20 1 (c) T3 promoter
448-2617 nmin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    653- 760 108- 1 (c) Blueks-polylinker 772- 791 20- 1 (c) T3 promoter 795-1031 237- 1 (c) puC19 1032-2964 2686- 754 (c) pUC19 Conflict (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue Source 3.458 5943-5488 (c) phage fl 460-624 236-400 purusce 626-645 1-20 T7 promoter 653-760 108- 1 (c) BlueKS-polylinke 795-2964 448-2617 puruscer 795-2964 (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VecBase(3):BlueKSm, VecBase(3):BlueSKp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phage fl
puc19
T7 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Successive Apriles and state of the state of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Features of BlueKSp (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Features of BlueKSp (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:32630"
736 c 755 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
5943-5488 (c) p
449- 285 (c) E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                          04-MAR-1987
03-APR-1987
    02-FEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               #parent
VecBase(3):BlueM13p
                                                                                                                                   בייטאערב artificial REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY BlueKSp
                                                                                     #sequence 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               residue
3- 458
460- 624
626- 645
        *sequence
                                                   *sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      750 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
```

```
Query Match 47.6%;
Best Local Similarity 88.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  GI:416305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ø
                                                                                                                                                                                                                                                                                                                                                                                                      U03436
U03436.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
XXU35136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                               LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                        11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                        RESULT
PRS304
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ð
                                                                                                                                                                                                                                           g
                                                                                                                                                                                                             δ
                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/product="chloramphenicol acetyltransferase"
/product="chloramphenicol acetyltransferase"
/product="chloramphenicol acetyltransferase"
/db_xref="c1:98409"
/translation="MEKKITGYTTVDISGWHRKEHFBAFQSVAQCTYNQTVQLDITAF
/translation="MEKKITGYATTVDISGWHRKEHFBAFQSVAQCTYNQTYQTIGTF
/translation="MEKKITGYTTVDISGWHRKEHFBAFQSVAQCTYVPHEQTEF
/translation="MEKKITGYTVDISGWHRKEHFBAFQSVAQCTYTVPHEQTEF
/schwerthpoffqcf=ftysqovAcvGsNLAYFPKGFTENMFFVSANPWVSFTSFDLNV
AMMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/transl_table=11
/product="ampicillin resistance"
/product="beta-lactamase"
/product="beta-lactamase"
/product="beta-lactamase"
/product="104400"
/product="104400"
/dxref="041:98490B"
/translation="ASIOHFRVALIPPFRARCLPVFRHPETLVKVKDAEDOLGARVGY
/translation="ASIOHFRVALIPPFRARCLPVFRHPETLVKVKDAEDOLGARVGY
readslation="ASIOHFRVALIPPFRARCLPVFRHPETLVKVKDAEDOLGARVGY
readslatinoGMTVRELCSAAITMSDWTAANLLITTIGGRKELTAFLHNMCDHVTRL
PRWEPELNBAIPNDERDTTMRVATTLRKLITGELLITASRQQLIDWMEADKVAGPL
LIRSALPAGWFIADKSGAGGERGSRGILAALGPDGKRPSRIVVITTGSGATMDERNRQIA
DRWEPELNEAIPNDERDTTWBVAMATTLRKLITGELLTLASROOLIDWMEADKVAGPL
LRSALPAGWFTADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"
                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (31-MG-1995) Paul N. Hengen, Laboratory of Mathematical
Submitted (31-MG-1905) Paul N. Hengerick, MD 21702-1201, USA
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cloning vector pBSL159.
Cloning vector pBSL159
Cloning vector pBSL159
I bases la sequence; vectors.
I (bases 1 to 4144)
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
General antibioutio-resistance gene cassettes and omega elements
for Escherichia coli vector construction and in vitro
deletion/insertion mutagenesis
deletion/insertion mutagenesis
SpSS4958
2. (1995)
                                                                                                                                                                                                               GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                   26-SEP-1995
                                                                                                                                                                              ö
                                                                                                                                          Length 3306;
                                                                                                                                                                                                                                                                                                                                                                                                                                      XXU35131 4144 bp DNA circular SYN
Plasmid pBSL159 cloning vector, complete sequence.
U35531
U35131.1 GI:984907
                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(3704. .4144,1. .219))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 4144,

/organism="Cloning vector pBSL159"

/plasmid="PBSL159"

/db_xref="taxon:42704"

complement(1129). 1989)

/EC_number="3.5.26"

/codon_start=1
                                                                                                                                          ; DB 14;
. 7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                    circular
                                                                                                                                        ; Score 69; DB 14
; Pred. No. 7e-12;
0; Mismatches
                                                                   862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 959 g
                                                                 790 g
                                                                                                                                                                                                                                                                                                  GGGGGCCTAACTAACTTTTGTT 130
                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIGASLIKHW"
                                                                                                                                              Query Match 47.6%;
Best Local Similarity 88.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1009 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hengen, P.N.
Direct Submi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1084 a
                                                                       854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
XXU35131
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                        106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                      셤
```

7

```
(bases 1 to 4267)
Stillman, D. J.
Stillman, D. J.
Submitsion
Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132, USA
City, UT Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cloning vector pBSL97.
Cloning vector pBSL97.
artificial sequence; vectors.
1 (bases 4289)
Alexeyev.M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omega elements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning vector pRS304.
Cloning vector pRS304
artificial sequence; vectors.
1 (bases 1 to 4267)
Sixorski.R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989)
                                                                                                  2726 GIGGAICCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACTCGAGG 2785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-1995
                                                                            46 GIGGAICCCCCCGGGCIGCAGGAAITCGATAICAAGCITAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                      PRS304 4267 bp DNA circular SYN 14-SEP-1995
Yeast integrative vector pRS304 with TRP1 marker, complete
Sequence.
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4267;
Length 4144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXU35136 4289 bp DNA circular SYN Plasmid pBSL97 cloning vector, complete sequence. U35136 U35136.1 GI:984923
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
47.6%; Score 69; DB 14;
Best Local Similarity 88.2%; Pred. No. 7.2e-12;
Matches 75; Conservative 0; Mismatches 10;
  Score 69; DB 14; L
Pred. No. 7.2e-12;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1981 GGGGGCCGGTACCCAGCTTTTGTT 2005
                                                                                                                                                                                            2786 GGGGCCCGGTACCCAGCTTTGTT 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GGGGCCTAACTAATTTTGTT 130
                                                                                                                                                                  106 GGGGCCTAACTAACTATTTTGTT 130
```

```
UT 84132, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2087 GGGGCCCGGTACCCAGCTTTTGTT 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2167 GGGGGCCGGTACCCAGCTTTGTT 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 GGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 GGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 4443)
Stillman, D.J.
        2 (bases 1 to 4373)
Stillman, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U03435.1 GI:416304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ದ
                                                                                                                                                                                                                                                                       ៧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89276910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1149
                                                                                                                                                                                                                                                                    1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
ASAJ5326/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE
                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
PRS303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="WIEDGDHAGSPAAWVERLEGYDWAQOTIGCSDAAVFRLSAQGR
/translation="WIEDGDHAGSPAAWVERLEGYDWAQOTIGCSDAAVFRLSAQGR
PVLEVKTDLSGALMELQDEAARLSWIATTGYPCAAVLDVYTEAGROWLLIGEVPGODL
LSSHLAPAEKVSIMADAMRRALHTDPATCPFDHQAKHRIERARTRMEAGLVDQDDLDE
EHQGLAPAELEARLEARMADCEDLVYTHGDACLPHINTWENGRESGFIDGGRLGVADDLD
ENDALATRDIAEELGGEWADRFLVLYGIAAPDSQRIAFYRLLDEFF"
COMPLEMENT(3)30.1.4161)
/CC_number="3:5.2.6"
/transl_tabl==11
/function="ampicillin resistance"
/function="ampicillin resistance"
/product="beta-lactamase"
/product="bet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                   Hengen, P.N.
Direct Submission
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vector pRS306.
Cloning vector pRS306
artificial sequence; vectors.
1 (bases 1 to 437)
Sikorski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2015 GIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 2074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GIGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACGTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1995
complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
for Escherichia coli vector construction and in vitro deletion/insertion mutagenesis Gene 160 (1), 63-67 (1995) 9534958 2 (bases 1 to 4289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 14; Length 4289;
Pred. No. 7.2e-12;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRS306 4373 bp DNA circular SYN
Yeast integrative vector pRS306 with URA3 marker,
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="neomycin phosphotransferase"
/protein_id="AAC53629.1"
/db_xref="G1:984924"
                                                                                                                                                                                                                                                                  1. .4289
/organism="Cloning vector pBSL97"
/plasmid="pBSL97"
/bd_xref="taxon:42709"
complement(804. .1598)
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2075 GGGGCCCGGTACCCAGCTTTTGTT 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 GGGGGCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:416307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             003438.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1024
                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
PRS306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                   MEDLINE
REFERENCE
                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
Direct Submission
Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning vector pRS303.
Cloning vector pRS303
artificial sequence; vectors.
1 (bases 1 to 4443)
Sikorski,R.S. and Hieter,P.
A system of Shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2027 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTTGACCTCGACCTCGAGG 2086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2107 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 2166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 GIGGATCCCCCGGGCIGCAGGAAITCGAIATCAAGCITATCGAIACCGICGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRS303 4443 bp DNA circular SYN 14-SEP-19
Yeast integrative vector pRS303 with HIS3 marker, complete
                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                 Length 4373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 47.6%; Score 69; DB 14; Length 44
Best Local Similarity 88.2%; Pred. No. 7.2e-12;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Cloning vector pRS303"
/db_xref="taxon:31826"
1 1048 c 1109 g 1137 t
                                                                                                                                                       1. .4373
/organism="Cloning vector pRS306"
/db_xref="taxon:31829"
a 987 c 1106 g 1099 t
                                                                                                                                                                                                                                                                                                                                                                 Query Match
47.6%; Score 69; DB 14;
Best Local Similarity 88.2%; Pred. No. 7.2e-12;
Matches 75; Conservative 0; Mismatches 10
```

us-08-935-377-6.rge

```
/protein_id="CaA06473.1"
/protein_id="CaA06473.1"
/db_xref="C1+028985"
/trailation="MFHIDTLATLYARTLILLGRKLVHSVSFLKKYTIPEPVAGGLL
/trailation="MFHIDTLATLYARTLILLGRKLVHSVSFLKKYTIPEPVAGGLL
/trailation="MFHIDTLATLYARTLILLGRAMSKLFEIERVGFFUVV
VILALLYIKKSMWHSVBASLGLDPPMAGLLAGSTILLGGGFGAANSKLFIERRGFNATEV
GLINWORAIGIGARSLIGLDPPMAGLLAGSTILLGGGAANSKLFIERRGFNATEV
AMACATFGLVLGGIGGPVARQLTLKGNKSWPOFPSRSTVSISLISNGSPOPLV
ERRPPPRNSSNSPSESTYSTRVKHSTTPNGIPDOEVPTAFEKPDVGRMITSLVLI
ERRPPPRNSSNSPSESTYSTRVKHSTTPNGIPDOEVPTAFEKPDVGRMITSLVLI
ERRPPPRNSSNSPSESTYSTRVKHSTTPNGIPALPMALILMLYQTIERRGFRAYS
VLGNVSLSLFLAMALMGIKLMELASLALPMALALLWUVQTIERALYALFTVTWALVIKL
AMVLAAGHGGGTGAATPATANMOAITERFGPSHMAFLVVPWVGAFFIDIVNALVIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                            Direct Submission
Submitted (03-APR-1998) Gal J., Institute for Biotechnology, Bay
Zoltan Foundation for Applied Research, Szeged, Derkovits fasor 2.,
6726, HUNGARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                    2 (bases 1 to 4670)
Gal,J., Szekeres,S., Schnell,R., Pongor,S., Simoncsits,A. and
Kalman,M.
                                                                                                                                                                                                                                                                                                                                                                   A positive selection cloning system based on the gltS gene of Escherichia coli Anal. Blochem. 266 (2), 235-238 (1999) 99107575
ASAJ5326 4670 bp DNA circular SYN 08-FEB-1999 pGAII(+) KS positive selection cloning vector gltS gene. AJ005326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

47.6%; Score 69; DB 14; Length 4670;
Best Local Similarity 88.2%; Pred. No. 7.2e-12;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
1. 4670
Aorganism-"synthetic construct"
/Organism-"synthetic construct"
/Organism-"synthetic construct"
/Organism-"synthetic construct"
/Organism-"synthetic construct"
/gene-"gits"
/gene-"gits"
/transl_table=1
/transl_table=1
/transl_table=1
                                                                                                           gits gene; glutamate permease.
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 4670)
Gal,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: May 29, 2000, 21:35:29 Job time: 36861 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1440 GGGGCCCGGTACCCAGCTTTTGTT 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1231 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 GGGGCCTAACTAACTATTTTGTT 130
                                                                                       AJ005326.1 GI:4028984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1165 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                   DEFINITION
                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
```

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

May 29, 2000, 21:58:11 ; Search time 1446.77 Seconds (without alignments) 25.075 Million cell updates/sec Run on:

US-08-935-377-6 145 1 GGCCAAAAATTGAAAAACTA......TTGTTTTGTGGGCCCGGCC 145

Title: Perfect score: Sequence:

Scoring table:

311585 seqs, 125096042 residues Searched: Total number of hits satisfying chosen parameters:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		Nucleotide analogu	leoti	탸	Human endogenous r	Human endogenous r	Plasmid pG+host4 c	teroidog	pG+host5	st		Ы	London-FAD APP tar	Swedish/London-FAD	Swedish-FAD APP713	Human endogenous r	bDAT. cDNA encodin	PRIPHA	coli biotin	731274 Seg	DE19731274 Seq ID	731274 Seq	731274 Seq		uman endog		Yeast RAD17 coding	Stealth virus nucl	. Stealth virus plas	ide sec	id pAT-1 se	<u> </u>	Nucleotide sequenc
	ID	987664	T04866	X20513	V31294	T75006	T75005	048463	T39485	048464	048465	V09028	X24730	X24731	X24732	X24733	V68808	026664	T43794	X02800	X02814	X02815	X02812	X02813	V57377	T75010	T91037	X01271	V10190	V12003	X05602	T04575	V22271	V69740
	图:	Н	-	-	Н	н	Н	Н	Н	н	-	Н	-	-	-	Н	~	Н	Н	-1	-		Н	-	Н	-	ч	н	Н	Н	-	Н	-	н
	Length	S	0	S	2	60	12	79	4226	23	72	052	281	69	569	570	54	4	35	84	46	œ	79	81	59	4	15	15	œ	Φ	4	9	4164	9
% Query	Match		۲.		46.2	46.2		46.2	46.2	46.2		46.2	9	٥	ė.	ė		ď.	45.1	4		44.8							٠	•		40.7	40.7	40.7
	Score	69	69	67	49	67	67	67	67	67	67	67	67	67	67	67	9	65.4	S	65	65	65	65	65	65	3	62.6	a	~	a	0	59	59	59
Result	No.	c 1	~	m		c S			œ		c 10	-	12	13	14	15	c 16	~	-	19	7	~	7	c 23	24	7	c 26	~	78	58	30	31	32	33

RESULT 2 T04866 ID T04866 standard; DNA; 501 BP. C T04866;

pret-Splice. Nucle Candida CaRhol gen Candida CaRhol gen Clone #4 from muta E. coli biotin DNA Plasmid pks varian plasmid pks/10 DN Plasmid pks/5 DNA Plasmid ppks/6 DNA Plasmid ppks/6 DNA Plasmid ppks/7 BNA Hybrid vector psr-DNA sequence of ex	
1149249 14992402 14992402 14992402 14992402 149255 149255 149255 149255 149255 149256 149256	
наннаннанна	
5178 3198 3198 4598 78 2973 3956 4088 4102 4583 10504	
4 w w w w w w w w w w w w w w w w w w w	
გოს 	
Ი ᲡᲡᲡᲡᲡᲡᲡᲡᲥᲥᲥᲥᲥ ᲥᲡᲘᲡᲡᲓᲔᲔപദᲡᲥᲡ	

## ALIGNMENTS

149

6

ပဲ 167

180 A;

```
106 GGGGGCC 112
                                                                                                                                                                                                                                                                                        138 GGGGGCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 GGGGGCC 6
651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Si
Matches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             음
                                                                                                                                                                                                                                                                                                                                                                                                         ð
                                                                                                                                                                                                        움
                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                          임
                                                                                                                                                                                                                                                                                                                                Modification of residual fluorescence labelled nucleotide analogues - to modification of residual fluorescence labelled nucleotide analogues - to prevent migration in electrophoretic sequencing gel and interference with base calling of DNA chains
FS Example. Fig 1. 18pp; Endish.

Example: Fig 1. 18pp; Endish.

Example: Fig 1. 18pp; Endish.

CC labelled nt analogues to prevent migration in electrophoretic labelled nt analogues to prevent migration in electrophoretic condification involves the use of a phosphatase enzyme to remove at modification involves the use of a phosphatase enzyme to remove at condification involves the use of a phosphatase enzyme to remove at conditionating kt. The template used was I microg. of M13 mp8. The configuration involves and phosphatase digestion. This confludes T04866. T04867 was a control nt. which was not treated with includes T04866. T04867 was a control nt. which was not treated with conditional phosphatase. The example shows that alkaline phosphatase control nt. which was not treated with the new part of the dye-terminator attefacts and allows for accurate base calling with the ABI analysis software.

Sequence 501 BP; 98 A; 136 C; 140 G; 121 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Figure 19.081273/07.

WPI: 99-081273/07.

New isolated Treponema pallidum nucleic acids - used to develop new isolated Treponema pallidum intections, characterisation, prevention products for the detection diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis Claim 1; Page 257; 1150pp; English.

X20500-2143 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JAN-1996 (first entry)
Nucleotide analogue treated with calf intestinal alkaline phosphatase.
Nucleotide analogue; alkaline phosphatase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Preponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 1; Length 501; Pred. No. 2.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Indels
                                                                                                                                                    /*tag= a
/note= "std. IUPAC codes used"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                     Location/Qualifiers
1. .501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 GGGGCCTAACTAACTATTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 GGGGCCCGGTACCCAGCTTTGTT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998.
23-JUN-1998; UJ3041.
24-JUN-1997; US-050667.
FIDAR-) HUMAN GENOME SCI INC.
Fraser CM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X20513 standard; DNA; 651 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 47.6%;
Best Local Similarity 88.2%;
Matches 75; Conservative
                                                                                                                                                                                                     Reeve MA, Robinson PS;
WPI, 95-328290/42.
Modification of residual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9859034-A2.
                                                                                                                                 misc_feature
                                                                                                                                                                                                   W09524505-A
                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
X20513
```

ò 쉱 ò В

NAME OF STREET O

```
28-MAY-1997; U21347.

PR 21-NOV-1997; U21347.

PR 14-OCT-1997; U21347.

PR 22-NOV-1997; U3-011626.

PR 22-NOV-1997; U3-011626.

PR (UYMI-) UNIV WISCONSIN.

PR (HUMA-) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMA-) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC.

PR (HUMAN GENOME SCI INC.) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0cr-1998 (first entry)
E. coli J96 pathogenicity island contig #108.
PAI: pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                           46 GIGGAICCCCCGGGCCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
T75006 standard; DNA; 1091 BP.

AC T75006; 1997 (first entry)
DT 06-0CT-1997 (first entry)
DE Human endogenous retroviral sequence 6.
KW Breast cancer; tumour; B18Ag1; prognosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.2%; Score 67; DB 1; Length 752;
100.0%; Pred. No. 1.3e-14;
Hive 0; Mismatches 0; Indels
                    Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 G;
                                DB 1; L(
1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 100.0%; Pred. No. 1.3 67; Conservative 0; Mismatches
                        46.2%; Score 67; DB 100.0%; Pred. No. 1.2 :ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 4
V31294/c
ID V31294 standard; DNA; 752 BP.
Query Match
Best Local Similarity lov..
Best 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       752 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 GGGGGCC 112
```

```
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 67; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3792 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3481 GGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGGGCC 112
            106 GGGGGCC 112
                                   48 GGGGCC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9629338-A1.
                                                                                                                           18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                              048463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                         RESULT
T39485
                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                    GIGGATCCCCGGGCTGCAGGAATICGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endogenous human tumour-associated retroviral element, B18Ag1 - used for the prognosis, diagnosis and monitoring of human cancers, especially breast cancer [Claim 10]. Page 30-31; 74pp; English.

Human endogenous retroviral sequences 10, 11-29, 3, 6, 12, 13, 14 and 11-22 (T75003-10) were obtd. by screening human genomic libraries using human breast tumour-associated retroviral element B18Ag1 (see also T75002) as probe. These non-contiguous sequences lie in order 11-22, 14, B18Ag-1, 13, 12, 10, 3, 11-29, 6 in the retrovirus sequences can be used in genetic vaccines and for the prognosis, diagnosis and monitoring of human breast cancer. Sequence 1122 BP; 260 A; 316 C; 185 G; 279 T;
                                                                                                    Endogenous human tumour-associated retroviral element, B18Ag1 - used
                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                            137 GIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCITAICGAIACGGICGACCICGAGG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    especially breast cancer claim displaying of human cancers, claim 10; Page 31-32; 74pp; English, 11-29, 3, 6, 12, 13, 14 and 11-22 (775003-10) were obtd. by screening human genomic libraries using human breast tumour-associated retroviral element libraries using human breast tumour-associated retroviral element BIBAg1 (see also 775001) as probe. These non-contiguous sequences ite in order 11-22, 14, BIBAg-1, 13, 12, 10, 3, 11-29, 6 in the retroviral sequences can be used in genetic vaccines and for the prognosis, diagnosis and monitoring of human breast cancer. Sequence 1091 BP; 79 A; 350 C; 97 G; 248 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-007-1997 (first entry)
Human endogenous retroviral sequence 3.
Breast cancer; tumour; B18Agl; prognosis; diagnosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.2%; Score 67; DB 1; Length 1122; 100.0%; Pred. No. 1.5e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                  Length 1091;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                Query Match 46.2%; Score 67; DB 1; Le Best Local Similarity 100.0%; Pred. No. 1.5e-14; Matches 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T75005/c
ID T75005 standard; DNA; 1122 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.(
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-1997; U00398.
10-JAN-1996; US-587329.
(CORI-) CORIXA CORP.
Frudakis IN, Smith JM;
                                   10-JAN-1997; U00398.
10-JAN-1996; US-587329.
(CORI-) CORIXA CORP.
                                                                          Smith JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 97-384982/35.
                                                                          Frudakis TN, Smit
WPI; 97-384982/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human retrovirus.
WO9725431-A1.
                                                                                                                                                                                                                                                                                                                                                                                                      106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                               77 GGGGGCC 71
                        7-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T75005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        φ
                                                                                                                                                                                                                                                                                                                                                     46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
õ
                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

```
Gruss A, Maguin E;

WPI; 93-303478/38.

WPI; 93-303478/38.

WPI; 93-303478/38.

WPI; 93-303478/38.

WPI; 93-303478/38.

We bacterial plasmid contg. heat sensitive replication system -
and marker gene, opt. capable of chromosomal integration, used to
inactivate specific gene or introduce heterologous gene
Example 2; FIG 9; 73pp; French.

SE Example 2; FIG 9; 73pp; French.

Contrologic resistance marker genes was subjected to mutagenesis with
hydroxylamine. A heat-stable mutant was isolated (coding for a heat-
contrologic resistance marker genes was subjected to mutagenesis with
hydroxylamine. A heat-stable mutant was isolated (coding for a heat-
contrologic resistance marker genes was subjected to an electric resistance marker genes was subjected to a least to a sensitive RepA = see Q48466 and Q48467, cut with Clai and Hpail and
t45bp PvuII fragment lacking the Cm resistance gene was ligated to a
t45bp PvuII fragment of pBluescript SK+ containing a multicloning
collection of the collectio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3541 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 3482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                               plasmid pG+host4 containing Is replication system.

Temperature sensitive replication; antibiotic resistance marker gene site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
Synthetic.
W09318164-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 96-443130/44.
Isolated human steroidogenesis acute regulatory protein gene - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; steroidogenesis; acute regulatory protein; hStAR; analysis; mutation; detection; prenatal, genetic defect; congenital; protein; lipoid adrenal hyperplasia; treatment; prevention; gene; replacement therapy; hypercholesterolaemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1997 (first entry)
Human steroidogenesis acute regulatory protein genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     742 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.2%; Score 67; DB
llarity 100.0%; Pred. No. 2.3
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1993, F00248.
12-WAR-1993; F00248.
13-WAR-1992; FR-003034.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-1996.
22-MAR-1995; U03896.
23-MAR-1995; US-410540.
(REGC ) UNIV CALLFORNIA.
(UYPE-) UNIV PENNSYLYANIA.
Lin D, Miller WL, Strauss JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1249 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T39485 standard; DNA; 4226 BP. T39485;
Q48463 standarc; DNA; 3792 BP.
```

```
Sequence
                                                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                     Matches
                                                                                                                                                                                                               46
                                                                                                                                                                                                                                                                                                4923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
          88888888888
                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                    ά
                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                                                                                                                 ö
for detection of mutation(s) of this gene that cause congenital

1 ipoid adrenal hyperplasia

2 Claim 1; Pages 23-25; 89pp; English.

2 Claim 1; Pages 23-25; 89pp; English.

2 Claim 1; Pages 23-25; 89pp; English.

2 Claim 2 Congenital 1; The hyperplasial (and page)

3 Congenital 1ipoid adrenal hyperplasia (CAH), or its

4 cransmission to children. CAH can be treated by protein or gene

3 Congenital 1ipoid adrenal hyperplasia (CAH), or its

4 cransmission to children. CAH can be treated by protein or gene

5 Cransmission to children. CAH can be treated by protein or gene

7 Phypercholesterolaemia.

8 A human adrenal cortex CDNA library was screened with a mouse StAR

8 Crasique protein. When it was cloned into pSPORT and expressed in

8 Cos-1 cells cotransfected with pP450scc abd pADX, it increased the

8 Consulpha hydroxycholesterol.
                                                                                                                                                                                                                                                                                                                                          4149 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 4208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B-MAR-1994 (first entry)
Plasmid pG+host5 containing Ts replication system.
Temperature sensitive replication; antibiotic resistance marker gene; site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cruss A, Maguin E;
WPI; 93-303478/38.

WPPI; 93-303478/38.

New bacterial plasmid contg. heat sensitive replication system -
New bacterial plasmid contg. heat sensitive replication, used to
inactivate specific gene or introduce heterologous gene
Example 2; Fig 10; 73pp; French.

Example 2; Fig 10; 73pp; French.

Plasmid pGK12 (Appl.Environ.Microbiol., 48; 726 (1984)) contg. two
plasmid pGK12 (Appl.Environ.Microbiol., 48; 726 (1984)) contg. two
antibiotic resistance marker genes was subjected to mutagenesis with
hydroxylamine. A heat-stable mutant was isolated (coding for a heat-
sensitive Repa - see Q48466 and Q48467), cut with Clal and HpaII and
the 3340bp fragment lacking the Cm resistance gene was ligated to a
445bp PvuII fragment of pBluescript SK+ containing a multicloning
                                                                                                                                                                                                                                                                                                                            46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a /standard_name= ORI /standard_name= ORI /note= "origin of replication from pBR322" 2640. .4383 /*tag= b /note= "from pGK12 (derived from pWV01)" 4384. .4786
                                                                                                                                                                                                                               984
                                                                                                                                                                                                                                                                      Length 4226;
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                1144 G;
                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                         DB 1; Le
2.4e-14;
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                  1132 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                         Score 67;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /.rag= c
/note= "from pUBll0"
4787. .5234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 36. .1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "from pSK"
                                                                                                                                                                                                                                   940 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        048464/c
ID 048464 standard; DNA; 5234 BP
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0%;
Matches 67; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                4209 GGGGGCC 4215
                                                                                                                                                                                                                                                                                                                                                                                      106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9318164-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 048464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                        ò
```

```
and marker gene, opt. capable of chromosomal integration, used to nactivate specific gene or introduce heterologous gene.

Inactivate specific gene or introduce heterologous gene.

Bisclosure; Fig II, 73pp; French.

Disclosure; Fig II, 73pp; French.

Corplaint of the state of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4983 GIGGAICCCCCGGGCIGCAGGAAIICGAIAITHIIHHHHHHHHHHHHHHHHHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pd-host6 containing Ts replication system.

Temperature sensitive replication; antibiotic resistance marker gensite-specific recombination; chromosomal integration; inactivation; beterologus gene expression; thermosensitive plasmid; ds.

Synthetic
site, T7 and T3 promoters and sequencing primer binding sites. The resulting plasmid was designated pVE6004 (or pG+host4 - 046463).
To facilitate cloning in B.coli, the 1.4kb Avai-AlwNI fragment of pBR322 (containing the origin of replication) was inserted into Nsir-cleaved pG+host4 to give pG+host5 (048464). The pBR322 ORI allows maintenance of the plasmid in E.coli at 37 deg.C. while the heat-sensitive ORI allows maintenance at 28 deg.C in gram-positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New bacterial plasmid contg. heat sensitive replication system
                                                                                                                                                                                                                                                                                                                       1559 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6722;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 5234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1503 G;
                                                                                                                                                                                                                                                                                                                       1133 G;
                                                                                                                                                                                                                                                                                                                                                                                                                               score 67; DB 1; Le
Pred. No. 2.6e-14;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Pred. No. 2.8 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1278 C;
                                                                                                                                                                                                                                                                                                                       973 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 46.2%; Scw
1 Similarity 100.0%; P:
67; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1961 A;
                                                                                                                                                                                                                                                                                                                               1569 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q48465 standard; DNA; 6722 BP. Q48465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ы
::
                                                                                                                                                                                                                                                                                                                                    5234 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gruss A, Maguin E
WPI; 93-303478/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6411 GGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1993
                                                                                                                                                                                                                                                                                              bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
```

```
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ME BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                     This is the nucleotide sequence of a clone of the fluory2 (fl2)
This is the nucleotide sequence of a clone of the fluory2 (fl2)

This is the nucleotide sequence of a 24-kDa alpha-zein protein (see W23977) that includes a 21-waino acid signal peptide (see W23976)
which targets the alpha-zein to the lumen of the rough endoplasmic reticulum. A claimed cereal plant contains a transgene comprising a first polynucleotide that encodes the fl2 signal peptide and a second polynucleotide that encodes an agronomically high-value contein. Also new are seeds produced by the plants, the transgene itself, and a transgene that also includes the fl2 promoter. The second polynucleotide preferably encodes a protein that has a high content of Mat, is, Try and/or Thr so that feeds from transformed maize, wheat, rice, barley, millet or sorghum will have increased contents of these essential amino acids in their seeds (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                             Cereal plants containing trans-gene expressing fusion that includes signal peptide of the fl2 maize gene - and protein having high content of essential amino acids, producing feeds of improved
                                                          20-JUL-1998 (first entry)
Maize fluory2 gene (fl2).
Floury2; fl2 gene: alpha-zein; signal peptide; transgenic plant; seed; essential amino acid; animal feed; maize; rice; wheat; barley; millet; sorghum; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2938 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 10529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2262 G;
                                                                                                                          Location/Qualifiers
1.760
/*tag a
/note= "vector-derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67; DB 1; Le
Pred. No. 3.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2484 C;
                                                                                                                                               .u. .3824
/*tag- b
/note- rolaim 14"
3825. .4613
/*tag- c
                                                                                                                                                                                                                                                                                                        (PION-) PIONEER HI-BRED INT INC. (UYAR-) UNIV ARIZONA STATE.

BEACH L. COLeman CE, Larkins BA; WPI: 98-110609/10.

P-PSDB; W23977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2845 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X24730 standard; DNA; 12814 BP. X24730;
                                         V09028 standard; DNA; 10529 BP
                                                                                                                                                                                                         .23. .3887
/*tag= d
3888
                                                                                                                                                                                                                                  /*tag= ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
                                                                                                                                                                                                                                                                                      11-JUL-1997; U11723.
17-JUL-1996; US-021833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 67; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10529 BP;
                                                                                                                                                                                                                                                                                                                                                                                             nutritional value
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111111
GGGGGCC 660
                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                            22-JAN-1998.
11-JUL-1997;
                                                                                                                                                                                                                                                                 WO9802563-A1
                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                            mat_peptide
                                                                                                                  Zea mays.
                                                                                                                                                                      promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          claimed)
                                                    V09028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X24730
ID X24730
AC X24730
                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46
                                                                                                                                                                                                   CDS
                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
```

```
Example: Page 56-103; 209pp; English.

This is the nucleotide sequence of Swedish-FAD APP targetting
This is the nucleotide sequence of Swedish-FAD APP targetting
This is the nucleotide sequence of Swedish-FAD APP targetting
strategy that facilitates the introduction of one or more specific
mutations into any gene in a single double reciprocal homologous
cecombination step. The method has been used particularly for
introducing a humanised amyloid precursor protein (APP) gene into
codents for producing animal models of Alzheimer's disease (AD).

Independent lines of transgenic mice (lines ESSOO7, ESSIO3,
Todents for producing animal models of Alzheimer's disease (AD).

Independent lines of transgenic mice (lines ESSOO7, ESSIO3,
Todents and ESSAO1) have been created using the gene targetting
technique applied to embryonic stem cells. In each line, the mouse
APP gene was modified to encode a mouse/human hybrid (m/hAPP) where
amino acid residues 666-770 of APP770 were encoded by human cDNA
sequences instead of mouse genomic exons (exons 16-18). Within
these residues, only a amino acid differences exist between the
mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr and
Arg-684 to His. The exon-cDNA fusion gene therefore encodes an APP
containing a humanised beta-amyloid domain. In line ESSOO7,
Created using vector pMTI-2398, the Swedish mutation. i.e.

KW(670,681) ML, was also introduced. The targetted Swedish FAD

M/hAPP gene expressed m/hAPP in brain.

Sequence 12814 BP; 1865 A; 1850 C; 1962 G; 1939 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9888 GIGGAICCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46 GIGGAICCCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p-FSDB; W97997, W97998.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
Swedish-FAD APP targetting vector pMTI-2398.
Amylold precursor protein; APP; human; gene targetting;
homologous recombination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pMTI-2398;
Swedish-FAD APP; mutation; ss.
Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.2%; Score 67; DB 1; Length 12814; 100.0%; Pred. No. 3.5e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUN-1999 (first entry)
London-FAD APP targetting vector pMTI-2453.
Amyloid precursor protein; APP; human; gene targetting;
                                                                                                                                                                                                                                                                                                                               /*tag- a
/standard_name= Swedish-FAD APP
/note= "encodes W97997"
5369. .6160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. nc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
/note= "encodes W97998"
                                                                                                                                                                                                                                                                  Location/Qualifiers
1932. .2276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X24731 standard; DNA; 15692 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.2
Best Local Similarity 100.
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
(FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 99-181029/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9948 GGGGCC 9954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wirak DO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
X24731
```

```
condon-FAD APP; Swedish-FAD APP; mutation; ss.
                                                                                                                                                                                     /*tag=
                                                                                                                 /*tag=
                                                                                                                                                                                                                                                         WO-U14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 67; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15692 BP;
                                                                                                                                                                                                                                           .8-AUG-1997; U14507
                                                                                                                                                                                                                                                                     FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12826 GGGGGCC 12832
                                                                                                                                                                                                                                                                                                 99-181029/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 GGGGCC 112
                                                                                                                                                                                                                 WO9909150-A1.
                Homo sapiens.
                                                                                                                                                                                                                                5-FEB-1999
                                                         mat_peptide
                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                         18-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                Synthetic.
                                                                                                                                                                                                                                                                                     Wirak DO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in brain
                                                                                                                                             mutation
                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                                        disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT: 15
X24733,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MERGE
    οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                            Example: page 104-113; 209pp; English.

Example: page 104-113; 209pp; English.

This is the nucleotide sequence of London-FAD APP targetting vector pMTI-2453. The invention provides a novel gene targetting vector pMTI-2453. The invention provides a novel gene targetting conditions into any gene in a single double reciprocal homologous mutations into any gene in a single double reciprocal homologous recombination step. The method has been used particularly for recombination step. The method has been used particularly for redents for producing animal models of Alzheimer's disease (AD).

Introducing a humanised amyloid precursor protein (APP) gene into created using the gene targetting s55401 and ES5403 have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse technique applied to embryonic stem cells.

ESS401 and ES5403) have been created using the gene targetting (m/hAPP) where amino acid residues 666-770 of APP770 were encoded by human cDNA sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 amino acid differences exist between the mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr and targetting a humanised beta-amyloid domain. In line ES5401, created using vector pWTI-2453, the London mutation i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qy 46 GIGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
Db 12766 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 12825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                     WPI; 99-181029/15.
P-PSDB; W97998, W97999.
Modification of target nucleic acids - by homologous recombination,
used particularly for introducing a humanised amyloid precursor
protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2541 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUN-1999 (first entry)
Swedish/London-FAD APP targetting vector pMTI-2454.
Amyloid precursor protein; APP; human; gene targetting; homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pMTI-2454;
    homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pMTI-2453; London-FAD APP; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

46.2%; Score 67; DB 1; Length 15692;
Best Local Similarity 100.0%; Pred. No. 3.8e-14;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2786 G;
                                                                                                                   /standard_name= "Swedish-FAD"
/note= "encodes W97999"
replace(4990,"")
                                                                                                                                                                 /*tag= b
/standard_name= "London-FAD"
8223. .9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2730 C;
                                                                                                                                                                                                                      /note= "encodes W97998"
                                                                           Location/Qualifiers
4807. .5151
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2423 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X24732 standard; DNA; 15692 BP.
X24732;
                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                 18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15692 BP;
                                                                                                                                                                                                                                                                                        (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 12826 GGGGGCC 12832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GGGGGCC 112
                                                     Homo sapiens
                                                                                                                                                                                                                                      WO9909150-A1
                                                                                 Key
mat_peptide
                                                                                                                                                                                             mat_peptide
                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                         Wirak DO;
                                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X24732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 XXXX BE GO
```

```
Example: Page 114-123; 209pp; English.

Example: Page 114-123; 209pp; English.

This is the nucleotide sequence of Swedish/London-FAD APP targetting vector part-245. The invention provides a novel gene targetting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous completely for introducing a humanised amyloid precursor protein (APP) gene into introducing a humanised amyloid precursor protein (APP) gene into introducing a humanised amyloid precursor protein (APP) gene into codents for producing animal models of Alzheimer's disease (AD).

Introducing a humanised amyloid stem cells. In each line, the mouse ES5401 and ES5403) have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse canno acid residues fof-770 of APP770 were encoded by human cDNA sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 mino acid differences exist between the mouse and human proteins, i.e. Gly-675 to Arg. Phe-681 to Thr and Arg-684 to His. The exon-CDNA fusion gene therefore encodes an APP containing a humanised beta-amyloid domain. In line ESS103, and the Swedish mutation. i.e. KW(670,671)ki, and the Swedish mutation. However here introduced. The targetted Swedish/London mutation. i.e. knowned in the appeted Swedish/London PADD MADP gene expressed introduced. The targetted Swedish/London PADD MADP gene expressed introduced. The targetted Swedish/London PADD MADP gene expressed introduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GIGGAICCCCCGGGCIGCAGGAATICGATAICAAGCITAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W97998, W98000.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            m/hAPP protein at levels approaching those observed for mouse APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2542 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 46.2%; Score 67; DB 1; Length 15692; I Similarity 100.0%; Pred. No. 3.8e-14; 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X24733 standard; DNA; 15701 BP.
X24733;
21-JUN (first entry)
Swedish-FAD APP713 targetting vector DMII-2454.
Amyloid precursor protein; APP; human; gene targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2783 G;
                                                                                                                                                                                                                                                     "Swedish-FAD"
                                                                                                                                                                                                                                                                                                                  /standard_name= "London-FAD"
8223. .9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2731 C;
                                                                                          /*tag= a
/note= "encodes W98000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encodes W97998"
Location/Qualifiers 4807. .5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2423 A;
                                                                                                                                                                   replace(4849,"")
                                                                                                                                                                                                                                                     /standard_name=
replace(4989,"")
```

```
Example: Page 124-133; 209pp; English.

Example: Page 124-133; 209pp; English.

This is the nucleotide sequence of Swedish-FAD APP713 targetting vector part-255. The invention provides a novel gene targetting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous crecombination step. The method has been used particularly for introducing a humanised amyloid precursor protein (APP) gene into introducing a humanised amyloid precursor protein (APP) gene into rodents for producing animal models of Alzheimer's disease (AD).

Introducing a humanised anyloid precursor protein (APP) gene into rodents for producing animal models of Alzheimer's disease (AD).

ES5401 and ES5403) have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse targetting to embryonic stem cells. In each line, the mouse candified to encoded a mouse/human pybrid (m/hAPP) where amyloid sesidues (66-770 of APP770 were encoded by human cDNA sequences instead of mouse genomic exons (exons 16-18). Within the mouse and human proteins, i.e. cly-676 to Arg, Phe-681 to The and Arg-684 to His. The exon-cDNA fusion gene therefore encodes an APP containing a humanised beta-amyloid domain. In line ES5215, created using vector pMTI-2455, the Swedish mutation. i.e. (RM(670,681)RL, was also introduced, and also a stop codon (T to sequence in the prosition of the containing and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wirak DO;
WPI: 99-181029/15.
P-PSDB; W97998, W98001.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pWTI-2455; Swedish-FAD APP713; mutation; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2845 G;
                                                                                                                                                                                                                                                                                     /standard_name= "Swedish-FAD"
replace(4981,"")
                                                                                                                                                                                                                                                                                                                                                               /standard_name= APP713stop
8232. .9032
/*tag= d
/note= "encodes W97998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2675 C;
                                                                                                                                                                                           /*tag= a
/note= "encodes W98001"
                                                                                                                                 Location/Qualifiers
4807. .4983
/*tag= a
                                                                                                                                                                                                                                        replace(4835,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2470 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999.
18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15701 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9909150-A1.
                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                        mutation
                                                                                                                                                                                                                                                                                                                  mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
```

Db 12775 GIGGATCCCCCGGGCTGCAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 12834 46 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105 0; Gaps Query Match 46.2%; Score 67; DB 1; Length 15701; Best Local Similarity 100.0%; Pred. No. 3.8e-14; Matches 67; Conservative 0; Mismatches 0; Indels ò

ö

106 GGGGGCC 112 ö

12835 GGGGGC 12841

Search completed: May 29, 2000, 21:58:21 Job time: 38169 sec

ar Q		and the second s	ే జ్ఞాన స్				
\$ 11. 8.					ż	3	
6.1 12.							
* * * *	• •					. •	
		w. Mar				er i es _j	
•							
						, ve	est.
				·			
			entre de la companya	· · · · · · · · · · · · · · · · · · ·			
							•
		and					
Ì							
						\$ 10 mm 1	The second secon
T.				9			
**************************************							
				•			

```
Sequence 121, App
Sequence 121, App
Sequence 1, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 56, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 113, App
Sequence 113, App
Sequence 5, Appli
Sequence 3, Appli
                                                               May 29, 2000, 22:08:54 ; Search time 621.83 Seconds (without alignments) 30.310 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                        145
1 GGCCAAAAATTGAAAACTA.....TTGTTTTTTGTGGGCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1
Sequence 1
Sequence 1
Sequence 2
                                                                                                                                                                                                                                                                                                               Issued_Patents_NA:*
1: /cgnl_6/ptodata//ina/5A_COMB.seq:*
2: /cgnl_6/ptodata///ina/5B_COMB.seq:*
3: /cgnl_6/ptodata///ina/5C_COMB.seq:*
4: /cgnl_6/ptodata///ina/6_COMB.seq:*
5: /cgnl_6/ptodata///ina/6_COMB.seq:*
6: /cgnl_6/ptodata///ina/PCTUS_COMB.seq:*
7: /cgnl_6/ptodata///ina/PCTUS_COMB.seq:*
7: /cgnl_6/ptodata///ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-967-101-121
US-08-952-541-121
US-08-302-752-1
US-08-410-540-3
US-08-410-540-3
US-08-302-752-3
US-08-302-752-3
US-08-992-334-3
US-08-992-334-3
US-08-992-334-3
US-08-992-334-3
US-08-198-446B-1
US-08-198-446B-1
US-08-198-446B-1
US-08-653-1556
US-08-957-101-113
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                         230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                            - nucleic search, using sw model
                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                            US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444444444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
67
67
67
                                           OM nucleic
                                                                                                                                    Seguence:
                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                   Database
                                                                   Run on:
                                                                                                             Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0000
```

Appl Appl Appl Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli Appli App		
		Gaps
sedneuce sed	តួ	93;
	RELATED	Length 7
	n US/08967101 E-HYSLOP, PETER H AUL E GENETIC SEQUENCES AND PROTEINS 183 S: 184 HURWITZ & THIBEAULT t TOWER - 125 High Street tts  M: Y disk compatible RC-DOS/MS-DOS RC-D	
707-7-118 707-1-118 707-1-118 707-1-118 708-1-118 708-1-118 708-1-118 708-1-118 708-1-118 708-1-118 708-1-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118 708-118	MENTS  H ES AND PRODISEASE  AULT  igh Street	DВ е-1
S-08-868-577-18 S-08-967-101-116 S-08-325-541-116 S-08-325-071-62 S-08-325-071-62 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-464-051-3 S-08-465-3 S-08-465-3 S-08-468-3	ALIGNMENTS 7101 PETER H COUENCES AN GER'S DISEA 125 High S 125 High S 7, 101	re 68.2; d. No. 2.7 Mismatches
-80 - SD -80	ALIGN  US/08967101  US/08967101  HYSLOP, PETER WHANNA M  ALZHEIMER'S  NALZHEIMER'S  NALZHEIMER'S  ALZHEIMER'S  ALZHEIMER'S  MAZHEIMER'S  ON SALZHEIMER'S  ON SA	Score Pred. 0; Mis
	n US/08 D-HYSLO JOHANNA JOHANN	4.8.
3 7480 7480 7480 7480 7480 7480 7480 7480	Itcation US/089671 CON: GEORGE-HYSLOP, P TION: TION: GENERIC SEO TION: THON: THON: THON: THON: THON: THON THON THON THON THON THON THON THON	47.0% 85.4% vative
######################################	THE NOTE OF THE NO	similarity 85 6; Conservativ
60008888888884444	1-121/c 21, Appl 2840240 NFCRMATHO NFCRMATHO NFCRMATHO NT: FRAM NT	Simi 6;
N 4444444 4 44 O,,,,,oooooooooooooooooooo	T. 1  19.967-101-121/C  JUDENCE 121, App  LEDT NO 1564054  APPLICANT: ST  APPLICANT: RO  CORRESPONDENCE  COUNTRY: BOSTO  STATE: MUSICANT: ROB  STATE: MUSICANT: ROB  COMPUTER READA  MEDIUM TYPE: DOPERATION  FILING DATE:  APPLICATION  FILING DATE:  APPLICATION  FILING DATE:  APPLICATION  FILING DATE:  APPLICATION  FILING DATE:  TELEPHONE: PICCATION  FILING DATE:  APPLICATION  FILING DATE:  TELEPHONE: CHARA  SEQUENCE CHARA  TOPOLOGY: 1  MOLECULE TYPE:  B-967-101-121	atc
00000000000000000000000000000000000000	RESULT 1  OS PORTOR  SEQUENCE  APPLIC COMPUT STAT COMPUT APPLIC A	Query Ma Best Loo Matches
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	A C C C C C C C C C C C C C C C C C C C	OHZ

```
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
CORRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
                                                                                                                                                                                                                                                                                     CURLENT APPLICATION DATE:

CARENT APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/0334
FILING DATE: 13-MAR.1992
ATTORNEY/AGENT INFORMATION:
NAME: PROULT, D. BILUCE
REGISTRATION NUMBER: 20958
REFERENCE/POCKET NUMBER: 20958
REFERENCE/POCKET NUMBER: CO93:31779
TELECOMMUNICATION INFORMATION:
TELEPHONE: (626) 795-9900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-08-302-752-1/c
Sequence 1, Application US/08302752
Patent No. 6025190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                             CITY: Pasadena
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: YES
; IMMEDIATE SOURCE:
; CLONE: pG+host4
US-08-992-334-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3481 GGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucle:
STRANDEDNESS
                                                                                                                                              91105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 coccensearccccccsccrscassarrcsararcaascrrarcsaraccsrcsaccrc 101
      42 CGCCGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08992334

Sequence 1, Application US/08992334

Patent No. 5919678

GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Gruss, Emmanuelle
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
TITLE OF INVENTION: PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47.0%; Score 68.2; DB 4; Length 793; 85.4%; Pred. No. 2.7e-14; tive 0; Mismatches 13; Indels (
                                                                                                                                                                                                                                                                                                APPLICANT: ST GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 GAGGGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 GAGGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                           102 GAGGGGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                62 cacceccecraccaccriricin 34
                                                                                                                                                                                                                       US-08-592-541-121/c
; Sequence 121, Application US/08592541
patient to 5986054
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: PITCHET, Edmund R.
TELECOMMUNICATION: TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic) US-08-592-541-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 85.4%
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massach
COUNTRY: U.S.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
US-08-992-334-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             엄
               ò
                                                     셤
                                                                                               ò
                                                                                                                                   셤
```

```
ö
                                                                                                                                                        3541 GIGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 3482
                                                                                                                        46 GIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCITAICGAIACCGICGACCICGAGG 105
                                                                  Gaps
                                                                  ö
Query Match

46.2%; Score 67; DB 4; Length 3792;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC COMPACIONS
SOFRATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.25 (EPO)
```

```
GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Gruss, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESSE: ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCATION: 1433..1434

COCATION: OTHER INFORMATION: /note= "interruption of sequence data"

CATION: 2208..2209

COCATION: /note= "interruption of sequence data"

FEATURE:
NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 2781..2782
OTHER INFORMATION: /note= "interruption of sequence data'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: 2956..2957
; OTHER INFORMATION: /note= "interruption of sequence data"
US-08-410-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-992-334-2/c
; Sequence 2, Application US/08992334
; Patent No. 5919678
    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Pasadena
STATE: California
COUNTRY: United States
                                                                                                   exon
1098..1283
                                                                                                                                                            exon
1620..1733
                                                                                                                                                                                                                    exon
2047..2174
                                                                                                                                                                                                                                                                             exon
2267..2425
                                                                                                                                                                                                                                                                                                                                      exon
2567..2751
                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
3031..3765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2956..2957
                                                                                                                                                                                                                                                                                                                                                                                                 exon
2328..2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3999 GGGGGCC 4005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: -
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                        NAME/KEY:
LOCATION:
                                                            ANTI-SENSE:
FEATURE:
                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08410540
Patent No. 5807678
GENERAL INFORMATION:
APPLICANT: Miller, Walter L.
APPLICANT: Lin, Dong
APPLICANT: Strauss III, Jerome F.
TILLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.2%; Score 67; DB 5; Length 3792; Best Local Similarity 100.0%; Pred. No. 1.1e-13; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTY: US

ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,540
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: 30,092
REFERENCE/DOCKET NUMBER: 30,092
TELEFAX: 415 853 5070
TELEFAX: 415 857 0663
TELEFAX: 380816COLDESTPA
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENTH: 4016 base pairs
                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PAPLICATION DATA:
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
PAPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
TYPE: nucleic acid
STRANDENNESS: 1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
FILING DATE:
                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-752-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 5 Palo A
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3481 GGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-410-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

ô

Gaps

```
46 GIGGAICCCCCGGGGCIGCAGGAATICGAIAICAAGCITATCGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3 Application US/08992334

Sequence 3 Application US/08992334

GENERAL INFORMATION:
APPLICANT: Gruss, Alexandra
APPLICANT: Maguin, Emmanuelle
TITLE OF INVENTION: PLASMID
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES:
CONTRESPONDENCE ADDRESS:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Sulte 500
                                                                                                                                                                                                                      Query Match
46.2%; Score 67; DB 5; Length 5234;
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Pasadena
STAME: 350 west Courage
CINTRY: Pasadena
STAME: California
STAME: California
COMPUTRY: United States
ZIP: 91108 1109
COMPUTRY: ENDABLE FORM:
MUDIUM TYPE: Floppy disk
COMPUTR: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PRE-BESS #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PR FR92/03034
FILING DATE: 12-MAR-1993
PRIOR APPLICATION NUMBER: PR FR92/03034
FILING DATE: 13-MAR-1993
PRIOR APPLICATION NUMBER: C93:31779
FILING DATE: 13-MAR-1993
PRIOR APPLICATION NUMBER: C93:31779
FILING DATE: 13-MAR-1993
PRIOR APPLICATION NUMBER: C93:31779
FILING DATE: C625 577-8800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: DOLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: DNA (genomic) US-08-992-334-3
                                                                                                 ; TOPOLOGY: linear
; MOLECULE IYPE: DNA (genomic)
US-08-302-752-2
SEQUENCE CHARACTERISTICS:
                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4923 GGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-992-334-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-302-752-2/C

Sequence 2, Application US/08302752

Sequence 2, Application US/08302752

Patent No. 6025190

TITLE OF INVENTION:

MUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION NATA:

APPLICATION NUMBER: US/08/302,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.2e-13;
Matches 67; Conservative 0; Mismatches 0; Indels
  ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
COMPOTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
FLING DATE: 17-DEC-1997
APPLICATION NUMBER: US 08/302,752
PRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: FR FR92/03034
ATMONEY/AGENT INFORMATION:
AND APPLICATION NUMBER: PR PR92/03034
ATMONEY/AGENT DEPLACED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C93:31779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: PEOUL, D. BEUCE
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:
TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDENESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: DNA (genomic) US-08-992-334-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4923 GGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
```

)

```
655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BETTAIN, RICHARD 3.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUBER: P1614-7007
TELECOMBUICATION INFORMATION: TELEPHONE: (202)638-5000
                                                        COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM IYPE: Flore
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA
US-08-793-610-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5714 GGGGGCC 5720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-198-446B-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                            ö
                                                                                                                        6471 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 6412
                                                                                                   46 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 105
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYBRIDS AND THE USE THEROF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                            ö
                 Length 6722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6722;
                 Query Match 46.2%; Score 67; DB 4; Length 672
Best Local Similarity 100.0%; Pred. No. 1.3e-13;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/302,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nikaido, Marmelstein, Murray & Oram LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Ler
1.3e-13;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
TITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.2%; Score 67; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 67; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US. 08-793-610-6
Sequence 6, Application US/08793610
Sequence 6, Application US/08793610
Sequence 6, Application US/08793610
SENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: STOCKING-HARBERS,
TITLE OF INVENTION: RETROVIRAL VECTOR HYE
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 672 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     US-08-302-752-3/c; Sequence 3, Application US/08302752; Patent No. 6025190; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: DNA (genomic) US-08-302-752-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                            6411 GGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6411 GGGGGC 6405
                                                                                                                                                                                     106 GGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                     ò
                                                                                                                                          g
                                                                                                                                                                                       ò
                                                                                                                                                                                                                          đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.1%; Score 65.4; DB 3; Length 9318; llarity 98.5%; Pred. No. 4.9e-13; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC STRBET: 1420 Fifth Ave., Suite 2800 CITY: Seatile STATE: WA
CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/793,610
FILING DATE: O'-MAR-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 94 4 31 973.8
FILING DATE: O'-FEP-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: O'-FEB-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AuG-1995
ATTORNEY/AGENT INFORMATION:

NAME: Berman, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08198446B
Patent No. 5674996
GENERAL INFORMATION:
APPLICANT: Hartwell Leland H.
APPLICANT: Weinert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Gooddine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
```

```
204 CGAAAATGATAAAATTGGGAAATTTGATCCATTTGAACAAATGGCATTTTAGGGGCTGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 CAAAAATTGAAAAACTAGATCTATTTATTGCACGGGGGGCGCCGTGGATCCCCGGGCTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 AGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSE: Christensen O'Connor Johnson Kindness PLLC STREET: 1420 Fifth Ave., Suite 2800 CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA

ZIP: 98101-2347

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,446B
FILING DATE:: 18-FEB.1994
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hartwell, Leland H.
APPLICANT: Welnert, Ted A.
APPLICANT: Welnert, Ted A.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62.6; DB 3;
Pred. No. 2.2e-12;
0; Mismatches 29;
                FILING DATE: May 14, 1992
APPLICATION WUMBER: US 0/882,051
FILING DATE: May 12, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR110798
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Shelhess, Dana K.
EKEGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FHCR17537
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
US 07/884,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-198-446B-10/c;
Sequence 10, Application US/08198446B
Patent No. 5674996
GENERAL INFORMATION:
                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1023 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 73.4%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA to mRNV
DESCRIPTION: Yeast RAD17
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-870-693-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 CGAAAATGATAAAATTGGGAAATTTGATCCATTTGAACAAATGGCATTTTAGGGGCTGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCGTGGATCCCCCGGGCTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Hartwell, Leland H.

APPLICANT: Hartwell, Leland H.

APPLICANT: Blon, Sharon E.

APPLICANT: Groudine, Mark T.

TITLE OF INVENTION: Cell Cycle Checkpoint Genes

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christensen O'Connor Johnson Kindness PLLC

STREET: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 AGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29; Indels
                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 18-FEB-1994

CLASSIFICATION: 536

ATTONNEY/AGENT INFORMATION:

NAME: Shelness, Diana K.

REGISTRATION NUMBER: FHCR17537

TELECOMMUNICATION NUMBER: PHCR17537

TELECOMMUNICATION INFORMATION:

TELEFAK: 206-224-0779

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: WA
ZIP: WA
ZIP: 98101-2347
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 73.4%; Pred. No. 2.2e-12;
Matches 80; Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DALE.
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,446
FILING DATE: February 18, 1994
APPLICATION NUMBER: PCT/US93/04458
TING DATE: May 12, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08870693
Patent No. 5866338
                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA to mRN.
DESCRIPTION: yeast RAD17
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1023 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORIGINAL SOURCE
) ORGANISM: Saurs-08-08-1466-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
```

ò 셤 ò g

)

```
204 CGAAAATGATAAAAATTGGGAAATTTGATCCATTTGAACAAATGGCATTTTAGGGGCTGC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCGTGGATCCCCCGGGCTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 2150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application US/08463115
| Sequence 56, Application US/08463115
| Patent NO. 5703221
| GENERAL INFORMATION:
| APPLICANT: WILLIAM JOHN MARTIN
| TITLE OF INVENTION: AND RELATED VACCINES
| STREET: 633 West 14th Street
| STREET: Suite 4700
| CITY: Los Angeles
| STATE: California CONVERT: Us. A.
| STATE: California CONVERT: Us. A.
| IP 90071-2066
| COMPUTER READALE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
| MEDIUM TYPE: Storage COMPUTER: IBM COMPATE: IBM P.C. DOS 5.0
| SOFTWARE: FastSeq Version 1.5
| COMPUTER: IBM COMPATION OF STATES INCLATION NUMBER: US/08/463,115
| FILING DATE: JUNE 5, 1995 |
| PRIOR APPLICATION DATA: Holuding application PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: 07/887,502 |
| FILING DATE: NO. 570321ember 23, 1993 |
| APPLICATION NUMBER: 07/887,502 |
| FILING DATE: NO. 570321ember 23, 1993 |
| APPLICATION NUMBER: 07/887,502 |
| APPLICATION NUMBER: 07/887,502 |
| APPLICATION NUMBER: 07/887,502 |
| APPLICATION NUMBER: 07/902 |
| APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43.2%; Score 62.6; DB 3; 1
llarity 73.4%; Pred. No. 2.8e-12;
Conservative 0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: September 20, 1991
ATORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISSTRATION NUMBER: 32,327
                     INFORMATION FOR SEC ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 2150 base pairs TYPE: nucleic acid STRANDEDNES: single TOPOLOGY: lines single TOPOLOGY: lines con to mena DESCRIPTION: yeast RADI7 CD HYPOTHETICAL: NO ANTI-SENSE: NO
206-224-0779
                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
741..1947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY;
; LOCATION;
US-08-870-693-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-463-115-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 CAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCGTGGATCCCCCGGGCTGC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 43.2%; Score 62.6; DB 1; Length 2150; Best Local Similarity 73.4%; Pred. No. 2.8e-12; Matches 80; Conservative 0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08870693
; Patent No. 5866338
; GENERAL INFORMATION:
APPLICANT: Hartwell, Leland H.
APPLICANT: Weinbert, Ted A.
APPLICANT: Plon, Sharon E.
APPLICANT: Groudine, Mark T.
TITLE OF INVENTION: Cell Cycle Checkpoint Genes
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Christensen O'Connor Johnson Kindness PLLC
STREEF: 1420 Fifth Ave., Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,693
                  SEQUENCE CHARACTERISTICS:
LENGTH: 2150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: yeast RAD17 cDNA
HYPOTHETICAL: NO
ARGINAL SOURCE:
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,446
FILING DATE: FEBRUARY 18, 1994
APPLICATION NUMBER: PCT/US93/04458
FILING DATE: May 12, 1993
APPLICATION NUMBER: US 07/884,426
FILING DATE: May 14, 1992
APPLICATION NUMBER: US 07/882,051
FILING DATE: MAY 12, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHCR110798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: FH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-682-8100
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: CDS
; LOCATION: 741..1947
US-08-198-446B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-870-693-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                        FEATURE
```

유 ö g

à

# # 10 T

REFERENCE/DOCKET NUMBER: 213/301
TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEFAX: (213) 955-0440
TELEFX: (7-3510
INFORMATION FOR SEQ ID NO: 56: SEQUENCE CHRACTERISTICS: LENGTH: 685 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear FEATURE: FEATURE: FEATURE: CUS-08-463-115-56

```
us-08-935-377-6.rni
```

```
        Query Match
        43.0%;
        Score 62.4;
        DB 2;
        Length 685;

        Best Local Similarity 94.0%;
        Pred. No. 2.3e-12;
        Matches 63;
        Conservative 0;
        Mismatches 4;
        Indels 0;
        Gaps 0;

        Qy 46 GTGGATCCCCGGGCTGGAGGATTCGAATTCGAATCGATATCGAAGCTTATCGAACCTCGAGG 105
        Interpretation 11 | Interpretation 12 | Interpretation
```

b₁

Title:

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 100.0
132 91.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş.
                                                                                                                                                                        (without alignments)
284.222 Million cell updates/sec
                                                                                                                                                                                                                                                                               145
1 GGCCAAAAATTGAAAAACTA......TTGTTTTTGTGGGCCCGGCC 145
                                                                                                                                              May 30, 2000, 09:48:27 ; Search time 2276.24 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cgnl_6/ptodata/1/pna/US085_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US086_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US086_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US087A_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US087C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US088A_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US088A_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US088C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US088C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US080C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US080C_COMB.seq:*
(Cgnl_6/ptodata/1/pna/US080C_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ptodata/1/pna/US090D_COMB.seq:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn1_6/ptodata/1/pna/US092A_COMB.seg:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                5142629 seqs, 2230885800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                    IDENTITY_NUC Gaport 1.0
                                                                                                                                                                                                                                                     US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                  score:
                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                 OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                   Run on:
```

```
cgnl_6/ptodata/1/pna/US0922_COMB.seq:*

cgnl_6/ptodata/1/pna/US0922_COMB.seq:*

cgnl_6/ptodata/1/pna/US092B_COMB.seq:*

cgnl_6/ptodata/1/pna/US093B_COMB.seq:*

cgnl_6/ptodata/1/pna/US093B_COMB.seq:*

cgnl_6/ptodata/1/pna/US093B_COMB.seq:*

cgnl_6/ptodata/1/pna/US093B_COMB.seq:*

cgnl_6/ptodata/1/pna/US093B_COMB.seq:*

cgnl_6/ptodata/1/pna/US094B_COMB.seq:*

cgnl_6/ptodata/1/pna/US001A_COMB.seq:*

cgnl_6/ptodata/1/pna/US6001A_COMB.seq:*

cgnl_6/ptodata/1/pna/US6001B_COMB.seq:*

cgnl_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgnl_6/ptodatta/1/pna/US06_NEW_COMB.seq.
/cgnl_6/ptodatta/1/pna/US07_NEW_COMB.seq.
/cgnl_6/ptodatta/1/pna/US08_NEW_COMB.seq.
/cgnl_6/ptodatta/1/pna/US09_NEW_COMB.seq.
/cgnl_6/ptodatta/1/pna/US09_NEW_COMB.seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ptodata/1/pna/PCT_NEW_COMB.seq:*/ptodata/1/pna/US06_NEW_COMB.seq
//ptodata/1/pna/US07_NEW_COMB.seq
//ptodata/1/pna/US07_NEW_COMB.seq
```

Sequence 6, Appli Sequence 7, Appli

US-08-935-377-6 US-08-935-377-7

28 28

145

SUMMARIES

Description

Gaps

; 0

```
61 IGCAGGAATICGATATCAAGCITATCGATACCGTCGACCTCGAGGGGGGGCCTAACTAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-935-377-7

Sequence 7, Application US/08935377

GENERAL INFORMATION:

APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: Tells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADERES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.C.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
STREET: 12006
COUNTY: Washington
STREET: Ploppy disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC Compatible
COURTER: IBM PC COMPATIBLE
COMPUTER: STEPEN: PC-DOS/MS-DOS
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/935,377
FILLING DATE: 22-SEP-1997
CLASSIFICATION: 424
ATTORNEY-AGENT THORMATION:
NAME: Steffe, Eric R
REGISTRATION NUMBER: 35,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 base pairs
TYPE: INCIDE: Caid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 145; DB 28;
Best Local Similarity 100.0%; Pred. No. 1.3e-38;
Matches 145; Conservative 0; Mismatches 0;
                                                                        1821.0010000/EKS/CMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TAATTTTGTTGTGGGCCCGGCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TAATTTTGTTTTTGTGGGCCCGGCC 145
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFRENCE/DOCKET NUMBER: 1821.
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 371-2600
TELEPAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 145 BASE PAIRS
TYPE: NUCleic acid
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE:
US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                              121, App
13627, App
8570, Ap
8523, App
8525, App
8625, App
862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2255,
Sequence 2255,
Sequence 2100,
Sequence 2100,
Sequence 2360,
Sequence 2360,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 108,
Sequence 996,
                                                                                                                                                                                                                                                                                                   Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6,
Sequence 6,
Sequence 6,
                                                                                                                                                                                                                                                                                                                                Sequence 12
Sequence 12
Sequence 12
Sequence 12
                                                                                                                        Sequence 4,
Sequence 91
Sequence 91
Sequence 91
Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sednence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
Sequence
Sequence
                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-935-377-6

Sequence 6, Application US/08935377

Sequence 6, Application US/08935377

GENERAL INFORMATION:

TILLE OF INVENTION: T Cells Specific for Target Antigens and TILLE OF INVENTION: Vaccines Based Thereon

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MORDING TIPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COERTAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 22.5EP-1997
              US-08-935-377-8
US-08-935-377-9
US-08-935-377-9
US-08-931-377-9
US-08-693-573-4
US-08-123-912-91
US-09-123-912-91
US-09-123-912-91
US-09-281-479-91
US-08-40-359-121
US-08-40-359-121
US-09-124-698-121
US-09-127-480-121
US-09-127-480-121
US-09-127-480-121
US-09-127-480-121
US-09-127-480-121
US-09-127-480-121
US-09-127-480-131
US-09-127-480-131
US-09-127-480-131
US-09-127-694-8595
US-09-127-694-8595
US-09-312-782-8595
US-09-312-782-8595
US-09-312-782-8595
US-09-312-782-8595
US-09-312-782-8595
US-09-312-782-8595
US-09-312-473-2334
US-09-328-351-2334
US-09-328-351-2336
US-09-328-351-2336
US-09-328-351-2336
US-09-328-351-2366
US-09-328-351-2366
US-09-328-351-2366
US-09-328-351-2366
US-09-328-351-2366
US-09-328-351-2366
US-09-328-351-2366
US-09-328-351-2366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New York
CITY: Washington
STATE: D. C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                   668.22.66
688.66
688.66
688.66
688.66
688.66
688.66
```

000000

ö g ò 8 ò g

```
56 CGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GGCCAAAAATTGAAAACTAGAICTATTTATTGCACGCGGCCGCCATGACGTGGATCCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GGCCAAAAATTGAAAAACTAGATCTATTATTGCACGCGCCGC----CGTGGATCCCC
                                                                                                   Sequence 9, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITTY Washington
STATE: D. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HOSOL, Shigeru, FUKAMI, Tadashi, HIYOSHI, Makiko TITLE OF INVENTION: Method of Determining Base Sequence of TITLE OF INVENTION: Nucleic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377 CLASSIFICATION: 4.44
ATTORNEY.AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION UNMBER: 36,688
REFERENCE/DGCKET NUMBER: 181.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cushman Darby & Cushman
STREET: Ninth Floor, 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 130; DB 28;
Pred. No. 1.4e-33;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 150
121 TAACTAATTTTGTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/08377383 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.78;
96.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.7
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                      US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-377-383-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ద
                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ï
                                                                                                                                                                                                                          61 GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGCCCCGAGGGGCGCCCAAC 120
                                                                                                                                                                                                     1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGAGTGGATCCCCC 60
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGCGCCC---GTGGATCCCCC 56
                                                                     Gaps
                                                                                                               1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCGCC---GTGGATCCCCCG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                     .,
ભ
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 149;
                         Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ENAPTY disk
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric R
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 basis
TYPE: NUCleic acid
TYPE: NUCleic acid
TYPE: NUCLEIC ASINGLE
                  Score 132; DB 28;
Pred. No. 2.9e-34;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 131; DB 28;
Pred. No. 6.3e-34;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 TAACTAATTTTGTTTTGTGGGCCCGGCC 145
                                                                                                                                                                                                                                                                                                              121 AACTAATTTTGTTTTTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                           118 AACTAATTTTGTTTTTGTGGGCCCGGCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.0%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.3%;
Best Local Similarity 97.3%;
Matches 145; Conservative
                                            Best_Local Similarity 98.0
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-935-377-8
                         Query Match
```

셤

셤 ö

5; Gaps

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Reed, Steven G.
APPLICANT: Read, Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 2101211.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR PELICATION NUMBER: 09/040,802
PRIOR PELICATION NUMBER: 09/040,802
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.0
SET ID NOS: LENGTH: 858
TYPE: DNA
CORGANISM: HOMO Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACGGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 GIGGATCCCCCGGGCTGCAGGAAITCGAIAICAAGCTIAICGAIAACCGTCGACCTCGAGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
47.6%; Score 69; DB 18; Length 22
Best Local Similarity 88.2%; Pred. No. 4.2e-13;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid Synthetic DNA US-08-693-573-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base
LOCATION: (711)
OTHER INFORMATION: Where n is a, c, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ο
δ
      FILING DATE: 25-JAN-1995
APPLICATION NUMBER: JP6911/1994
FILING DATE: 26-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Thomas G. Wiseman
REGISTRATION NUMBER: 35046
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ù
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-123-912-91
Sequence 91, Application US/09123912A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGGGCCTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 GGGGCCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (570)
OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
LOCATION: (591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                              TELEPHONE: (202)861-3000
TELEFAX: (202)822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (683)
OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
LOCATION: (570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08693573
GENERAL INFORMATION:
APPLICANT: HOSSI, Shigeru,
APPLICANT: FURAMI, Tadashi,
APPLICANT: COLIMA, Makiko
TITLE OF INVENTION: Method of Determining Base Sequence of
TITLE OF INVENTION: Method of Determining Base Sequence of
NUMBER OF SEQUENCES:
ADDRESSEE: UNTELLECTUAL PROPERTY GROUP OF
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: Ninth Floor, 1100 New York Avenue, N.W.
CITT: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 88.2%; Pred. No. 4.2e-13;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Diskett, 3.5 inch, 720Kb storage OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 or ASCII editors SOFTWARE: WordPerfect 5.1 or ASCII editors SOFTWARE: WordPerfect 5.1 or ASCII editors CURRENT APPLICATION DATA:

FILING DATE: 25-JAN-1995

CLASSIFTCATION NUMBER: UP6971/1994

FILING DATE: 26-JAN-1994

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....um TYPE: Diskette, 3.5 inch, 720Kb storage COMPUTER: IBM PC/XT/AT compatibles OPERATING SYSTEM: MS-DOS SOFTWARE: WordPerfect 5.1 or ASCII editors APPLICATION DATA: APPLICATION NUMBER: US/08/693,573 FILING DATE: 07-AUG-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid Synthetic DNA
US-08-377-383-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/693,573
FILING DATE: 07-AUG-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/377,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGGCCTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GGGGCCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Distriction
STATE: COUNTRY: USA 2005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
US-08-693-573-4
```

ద δ g

ŏ

ö

ö

ö

ö

```
; LOCATION: (820)
; OTHER INFORMATION: Where n is a, c, g or
US-09-221-107-91
                   ο
                                                                                                                                                                                                                                                                                                                                                       ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ú
                                                                                                                                                                                                                   ú
                                                                                                                                                                                                                                                                                                                                                                                                                        ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ú
                                                                                  ũ
                   ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
                                                                                  ď
                                                                                                                                                  ģ
                                                                                                                                                                                                                   ď
                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ส
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Where n is
                                                              LOCATION: (655)
OTHER INFORMATION: Where n is
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
            OTHER INFORMATION: Where n is
                                                                                                                                                ţs
                                                                                                                                                                                                               OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                   ^{1s}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
LOCATION: (777)
OTHER INFORMATICN: Where n
                                                                                                                                  LOCATION: (664)
OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Where n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified_base LOCATION: (787)
                                                                                                          NAME/KEY: modified_base
LOCATION: (664)
                                                                                                                                                                                                                                             NAME/KEY: modified_base LOCATION: (683)
                                               NAME/KEY: modified_base
                                                                                                                                                                              NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified_base
LOCATION: (760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified_base
                                                                                                                                                                                                   COCATION:
                                                                                                                                                                                                                                                                                                                                      COCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 91, Application US/09221107
GENERAL INFORMATION:
APPLICART: Wang, TONGTONG
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C2
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-11-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 68.6; DB 40; Length 858; Pred. No. 8.2e-13; 0; Mismatches 14; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Where n is a, c, g or t US-09-123-912-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                  g or
                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Where n is a, c, NAME/KEY: modified_base
LOCATION: (809)
                                                                                                                                                                                INFORMATION: Where n is a, c,
                                                                                                                                                                                                                                    ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION: Where n is a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION: Where n 1s a, c,
                                                                              OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                               TION: (765)

* INFORMATION: Where n is a, KEY: modified_base nonitied_ton.
                                                                                                                                                                                                                                                                                                                                      ಥ
                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (570)
OTHER INFORMATION: Where n is a,
FEATURE:
                                                                                                                                                                                                                                                                                     ď
                                                                                                                                                                                                                               INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                            R INFORMATION: Where n is
/KEY: modified_base
(ION: (801)
                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Where n is
NAME/KEY: modified_base
LOCATION: (804)
             LOCATION: (759)
OTHER INFORMATION: Where n is
NAME/KEY: modified_base
LOCATION: (760)
                                                                                                                                                                                                                                                                                  R INFORMATION: Where n is //KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 84.6%;
Matches 77; Conservative (
                                                                                                                                                                                                /KEY: modified_base
ilon: (787)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified_base
LOCATION: (820)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base LOCATION: (570)
                                                                                                                                                                                                                                                'KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified_base
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-221-107-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 91
LENGTH: 858
```

ò 셤 ö g ä

ö

```
42 CGCCGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 121, Application US/08496841

GENERAL INFORMATION:
APPLICANT: St. George-Hyslop, Peter
APPLICANT: Rommens, Johanna M.
APPLICANT: Fraser, Paul E.
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841
FILING DATE: 28-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 85.4%; Pred. No. 1.1e-12;
Matches 76; Conservative 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Testa, Hurwitz & Thibeault
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 GAGGGGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GAGGGGGGCCCGGTACCCAGCTTTTGTT 34
APPLICATION NUMBER: US/08/431,048A FILING DATE: 28-APR-1995
                                                                                   NAME: TWOMEY, MICHAEL J
REGISTRATION NUMBER: 38.349
REFERENCE/DOCKET NUMBER: CAN-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 28-JUN-1995
CIASSIFICATION: 424
ATTORNEY/AGBMT INFORMATION:
NAME: Twomey, Michael J
REGISTRATION NUMBER: 38349
TELECOMMUNICATION UNFORMATION:
TELEPHONE: (617) 248-7362
TELEFAX: (617) 248-7362
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE: CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-431-048A-121
                                        ATTORNEY/AGENT INFORMATION:
NAME: TWOMEY WITH
                                                                                                                                                                                                                                                                               : 793 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                            FILING DATE: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Tes
STREET: High S
CITY: Boston
STATE: Massacl
COUNTRY: U.S.A
ZIP: 02110
                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-08-496-841-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-496-841-121
                                                                                                                                                                                                                                                                                  CENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 333 aacgaattccaccacactggactagtggatcccccgggctgcaggaattcgatatcaagc 392
                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 ATCTATTTATTGCACGCGGCCGCCGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGC 81
                                                      Gaps
                                                                                                    22 AICIAITIAITGCACGCGGCCGCGTGGAICCCCCGGGCTGCAGGAAITCGAIAICAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-431-048A-121/c

Sequence 121, Application US/08431048A

Sequence 121, Application US/08431048A

GENERAL INFORMATION:

APPLICANT: ST. GEOGE-HYSLOP, PETER H

APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 132

CORRESPONDENCES. 132

CORRESPONDENCES. 132

ADDRESSEE: Patent Administrator, TESTA, HURWITZ &

ADDRESSEE: THIBEAULT, LLP

STREET: 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 858;
           Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                             Sequence 91, Application US/09285479
Sequence 91, Application US/09285479
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVEWIION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVEWIION: LUNG CANCER
FILE REFERENCE: 210121.45503
CURRENT APPLICATION NUMBER: US/09/285,479
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FASESO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPAtible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
47.3%; Score 68.6; DB 46;
Best Local Similarity 84.6%; Pred. No. 8.2e-13;
Matches 77; Conservative 0; Mismatches 14;
       Query Match
47.3%; Score 68.6; DB 43;
Best Local Similarity 84.6%; Pred. No. 8.2e-13;
Matches 77; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 TTATCGATACCGTCGACCTCGAGGGGGGCCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 ttatcgataccgtcgacctcgaggggggcc 423
                                                                                                                                                                                                                      82 TTATCGATACCGTCGACCTCGAGGGGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEI: misc_feature
; LCCATION: (1)...(858)
; OTHER INFORMATION: n = A,T,C or G
US-09-285-479-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                         ద
                                                                                                           à
                                                                                                                                                                                                   ö
```

```
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-124-523-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                           42 CGCCGTGGATCCCCCGGGCTGCAGAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CGGGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGTCGCGTC 63
                                                                         ö
                                     Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 793;
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: High Street
CITY: BOSTON
                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/509,359 FILING DATE: 31-JUL-1995 CLASSIFICATION: 800
                                 Score 68.2; DB 16;
Pred. No. 1.1e-12;
0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.0%; Score 68.2; DB 17;
85.4%; Pred. No. 1.1e-12;
tive 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 GAGGGGGGCCTAACTAACTTTTGTT 130
                                                                                                                                                                                       102 GAGGGGGGCCTAACTAACTAATTTTGTT 130
                                                                                                                                                                                                            62 GAGGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-08-509-359B-121/c
; Sequence 121, Application US/08509359B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    RESULT 12
US-08-509-359-121/c
Sequence 121, Application US/08509359
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEFHONE: (617) 248-7362
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 BASE PAIRS
TYPE: NUCleic acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Twomey, Michael J
REGISTRATION NUMBER: 38349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) US-08-509-359-121
                                   Query Match
Best Local Similarity 85.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.23
Best Local Similarity 85.49
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02110
                                                                                                                                                     ద
                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

```
42 CGCCGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 CGGGGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATATCGATACGTCGTC 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.0%; Score 68.2; DB 17; Length 793; 85.4%; Pred. No. 1.1e-12; tive 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121, Application US/09124523
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASE, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: IESTA, HURWITZ & THIBEAULT
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                    ADDRESSEE: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK STREET: 600 South Avenue West CITY: Westfield STATE: Wew Jersey COUNTY: U.S.A. 2IP: 07090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: "High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word, Version 6.0c
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/509,359B
FILLING DATE: 31-JUL-95
CLASSIFICATION: 530
ATTORNEY/ACTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 GAGGGGGGCCTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 GAGGGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110 '
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Palisi, Thomas M.
REGISTRATION NUMBER: 36629
TELECOMMUNICATION INFORMATION:
TELEPAX: (908) 654-500
TELEPAX: (908) 654-7866
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGHI: 793 base pairs
LENGHI: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) MOLECULE TYPE: DNA (genomic) US-08-509-359B-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 85.4
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
```

```
q
                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
47.0%; Score 68.2; DB 40; Length 793;
Best Local Similarity 85.4%; Pred. No. 1.1e-12;
Matches 76; Conservative 0; Mismatches 13; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ST. GERGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: SENGENCE SENGENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEDUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: HIGH Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 GAGGGGGGCCTAACTAATTTTGTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GAGGGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                         US/09/124,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-121-698-121/c
; Sequence 121, Application US/09124698
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-124-523-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 793 base pairs
  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ογ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
```

```
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
```

Ţ**		0.00		· · · · · · · · · · · · · · · · · · ·		
A.		₩				
3			•			
d"						₹
5.5	•					
	•					
**						1.
			•			
-3		J. Oa				·
¥.			•			en e
i.						
			4			·
			\$ 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1 & 1			
			en e			
		en e				
		•				
*				• · · · · · · · · · · · · · · · · · · ·		
		*				
	4					*
		i i i i i i i i i i i i i i i i i i i				
				51 S	* .	
		14 1				
				¥ .		
			**			
		grant and a second				•
		n in the second		er ²		
			markan di Salaharan di Salahara			
			Sw ₁₄ A	*	<u> </u>	•
		* · · · · ·				
				Next endowed		e de la companya de
						<b>愛</b> 養.
			A STATE OF THE STA			
£.						
			in the second se	* · · · · · · · · · · · · · · · · · · ·		
<b>9</b>						AND
*						
5						
ps.C.						
<u>'.</u>						
<b>F</b>						
· .	en e	<i>t</i>			ar en	

gb_est27:*

gb_est28:*

gb_est28:*

en_est20:*

en_est21:*

gb_est31:*

gb_est31:*

en_est23:*

en_est23:*

en_est24:*

em_est25:*

gb_est31:*
gb_est33:*
gb_est36:*
gb_est35:*
em_est27:*
em_est27:*

Seguence:

Run on:

Searched:

em_est29

7

```
May 29, 2000, 21:13:13; Search time 2192.43 Seconds (without alignments) 268.067 Million cell updates/sec
                                                                US-08-935-377-6
145
1 GGCCAAAATTGAAAACTA.....TTGTTTTGTGGGCCCGGCC 145
                                                                                                                        9714632
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                           4857316 seqs, 2026611650 residues
                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                              OM nucleic - nucleic search, using sw model
                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                    em_est1::
em_est2::
em_est4::
em_est5::
em_est5::
em_est6::
em_est10::
em_est10::
em_est11::
em_est11::
em_est11::
em_est11::
em_est11::
em_est11::
em_est11::
em_est11::
                                                                                                                                                                                                                                                                                                                                                                                           gb_est15:*
gb_est16:*
gb_est17:*
                                                                                                                                                                                                                                                                                                                   9b_est3:*
9b_est4:*
9b_est5:*
9b_est6:*
9b_est7:*
9b_est7:*
9b_est9:*
                                                                                                                                                                                                                                                                              em_est16:*
em_est17:*
em_est18:*
em_est19:*
gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                    gb_est11:*
gb_est12:*
gb_est13:*
                                                                                                                                                                                                                                                                                                                                                                                                              gb_est18:*
gb_est19:*
                                                                                                                                                                                                                                                                                                                                                                                       gb_est14:*
                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est23:9
gb_est24:
                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est20:
                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est22;
                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est21
                                                                                                                                                                               EST:*
                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                          Scoring table:
                                                                                                                                                                              Database :
```

em_est30 9D_est410::* 9D_est41::** 9D_est42::** 9D_est44::** 9D_est44::** em_est31:** em_est33:** em_est34:** em_est34:** em_est34:** em_est34:** em_est34:** em_est33:** em_est47:** em_est47:* em_est4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_gss13:*
gb_gss14:*
gb_gss15:*
gb_gss16:*

em_gss11: em_gss12: gb_gss12: em_gss10:

em_gss4.*

gb_gss5.*

em_gss6.*

em_gss6.*

em_gss7.*

em_gss7.*

em_gss7.*

em_gss8.*

em_gss8.*

em_gss8.*

em_gss8.*

SUMMARIES

Department of Eukary The Institute for Ge 9712 Medical Center	Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tlgt. Clones are available end search page: http://www.tlgt.org/	Sed Files. M2 21 Class: BAC ends. FEATURES Location/Qu Source 1.682	/organism= /db_xrefa /clone="23" /clone_lib= /sex="Male"	/cell_type= /note="Vect HindIII" BASE COUNT 156 a 187 c ORIGIN	Query Match Best Local Similarity 93.6%; Matches 73; Conservative	Qy 46 GIGGAICCCCGGGCIGCAGGA	Qy 106 GGGGCCTAACTAA 12: 	RESULT 2 AQ009167/c LOCUS LOCUS DEFINITION CIT-HFP-2281N13.TF	genomic survey sequivactions and sequivaction accepted to the sequivaction accepted to the sequivaction and sequivactions accepted to the sequivaction accepted t	ORGANISM Homo sapiens Eukaryota; Metazoa; Eutheria; Primates; REFERENCE 1 (bases 1 to 608) AITHORS Adams M.D., ROUDISE		Contact: Mark Adams Department of Eukar The Institute for G 9712 Medical Center 701: 301 838 0200 Fax: 301 838 0208	Email: mdadams@tigr Clones are availabl end search page: http://www.tigr.org Seg primer: Ml3-21;	FEATURES CLASS: BAC GIUGA, CANDON CONTROL CONT
Description	AQ074693 CIT-HSP-2 AQ009167 CIT-HFP-2 B69688 CIT976SK-A- B54292 CIT-HSP-201 AU037147 AU037147 B95279 CIT-HSP-217	B80294 CIT-HSP-204 AQ013255 CIT-HSP-2 AQ041198 CIT-HSP-2 T48593 ph6f4_19/1T	AA052885 T3531 Blo B74162 CIT-HSP-202 AQ014512 CIT-HSP-2 B6534 CIT-HSP-202 A0012629 CIT-HSP-2	AQ012216 CIT HSP-2 AQ01221 CIT HSP-2 AQ001221 CIT HSP-2 B6406165 CIT HSP-2 B64363 CIT HSP-202 B70299 CIT HSP-202 AQ016737 CIT HSP-2	B66775 CIT-HSP-205 B80296 CIT-HSP-204 AQ009153 CIT-HSP-2 AQ074695 CIT-HSP-2	AA/321/2 9053043 AQ008437 CIT-HSP-2 AQ014519 CIT-HSP-2 B72088 CIT9785K-13	AQ012365 CIT-HSP-2 T26395 AB161A4F IN B26269 F10B5TF IGF A1239372 SWOVAFCAP	B53695 CTT-H8P-201 AQ003238 RPCI11-19 AA72115 96BS0066 U68746 Riftla pach AI058116 SWAMACI5 B65391 CTT-HSP-202	AQ024018 CPGR0359A AQ023564 CPGR0482A AQ023548 CPGR0051A AQ024077 CPGR0415A AQ024077 CPGR0415A		GSS 20-AUG-1998 apiens genomic clone 2301L23,	Craniata; Vertebrata; Mammalia; . Hominidae: Homo.	10	
ΩI	AQ074693 AQ009167 B69688 B54292 AU037147	B80294 AQ013255 AQ041198 T48593	AA052885 B74162 AQ014512 B65534	AQ012216 AQ01221 AQ002165 B64363 B70299 AQ016737	B68775 B80296 A0009153 A0074695			B53695 AQ003238 AA752115 RPU68746 AI058116 R65391			о <b>иа</b> SP Ношо s	data; Cr	. ਦੇ ਹ ਜ ਜ	
Length DB	1			547 575 575 596 596 607 632 84							682 bp 1123.TF CIT-) vey sequence	GI:34368	to 682) Rounsley ranger, D.	g (1998) rk Adams
Query Match Ler	44444 8884 8000 8000 8000 8000 8000 800	9999	00000	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	2444 2008 2008 2008	24 44 4 20 20 20 40 20 40 40 40	42.9 41.9 41.4	8888888 999999 99646	, , , , , , , , , , , , , ,	37.9	174693 -HSP-2301	AQ074693 AQ074693.1 GI:3436811 GSS. human. Homo sapiens Eukaryota; Metazoa; Chori	(bases 1 tans, M.D., rry, K., G.)	p Buildin published ntact: Ma
Score	67 . 4 67 . 4 67 . 67	79 79 79	60 67 67 67	700 700 700 700 700 700 700 700	65 79 79 79 79	65.4 65.4 85.4	62.2 60.8 60.8	7.7.2 8.7.7.2 4.7.2 6.8	ក សម្មាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស់ សម្គាស សម្គាស សម្គាស សម្គាស ស សម្គាស សម្គាស ស ស ស ស ស ស ស ស ស ស ស ស ស ស ស ស ស ស	55 55	1 3/c AQO ION CIT	STON AQO ON AQO ON AQO ON AQO ON AQO ON AQO ON AQO	63.70	
Result No.	000 C		000	c 118 c 118 c 129			0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0			A 4 5	RESULT 1 AQ074693/C LOCUS DEFINITION	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE	JOURNAL

```
٠.,
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gr.org
ble from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rg/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                     ..org
e from Research Genetics (info@resgen.com). BAC
                                                                                                                          //tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /,
Ley,S.D., Fleld,C.E., Bass,S., Linher,K.,
X., Granger,D., Suh,E., Wible,C., Kim,U.-J.,
M. and Venter,J.C.
End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp DNA GSS 27-JUN-1998 CIT-HSP Homo sapiens genomic clone 2281N13, puence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                          e-"Sperm"
ctor: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                      %; Score 70; DB 96; Length 682;
%; Pred. No. 1.7e-13;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-2281N13.TR.1 CIT-HSP-2281N13.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ms
aryotic Genomics
: Genomic Research
:er Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                          1 others
yotic Genomics
senomic Research
: Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                        151 t
                                                                                                                                                                                                            n="Homo sapiens"
-"taxon:9606"
2301L23"
|b="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Qualifiers
                                                                                                                                                                               qualifiers
                                                                                                                                                                                                                                                                                                                                            187 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23
```

```
Best Local Similarity 98.6%;
Matches 68; Conservative (
                                                                                                                  106 GGGGGCCTA 114
                                                                                                                                   106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 GGGGGCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                 RESULT
B54292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            쉺
                                                                                g
                                                                                                                  ö
                                                                                                                                               원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Unpublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Fibroblast"
/cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
/calTech Human BAC Library A"
125 t
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                B69688 528 bp DNA GSS 18-JUN-1998
CIT978SR-A-448E10.IVC CIT978SK HOMO SAPIENS GENOMIC Clone A-448E10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shruya, H., Simon, M. and Venter, J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                              Gaps
 /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="2281N13"
/clone_lib="CIT-HSP"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                    Length 608;
                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                Ouery Match
46.9%; Score 68; DB 96; I
Best Local Similarity 100.0%; Pred. No. 8.1e-13;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                   137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers

1. 528
/organism-Homo sapiens"
/db_xref="GDB:5299607"
/db_xref="taxon:9606"
/clone="A-448E10"
/clone=lib="CIT978SK"
                                                                                                                                                 166 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence.
B69688
B69688.1 GI:2708912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Female"
                                                                                                                                                    164 c
                                                                                                                                   HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                               106 GGGGGCCT 113
                                                                                                                                                                                                                                                                                                                                                                                 GGGGGCCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
B69688/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                              요
                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                               g
```

```
Homo sapiens
Eutheria, Primates; Craniata; Vertebrata; Mammalia;
Eutheria, Primates; Catarrhini; Hominidae; Homo.

Eutheria, Primates; Catarrhini; Hominidae; Homo.

Eutheria, Primates; Catarrhini; Hominidae; Homo.

E (Dases 1 to 108)

S Adams, M. D., Rounsley, S. D., Field, C. E., Bass, S., Linher, K.,

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,

Simon, M. and Venter, J. C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building

Unpublished (1997)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

Hominia and Adams are available from Research Genetics (info@resgen.com). Hatti
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46 GIGGAICCCCCGGGCTGCAGGAATICGAIAICAAGCITAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                               Gaps
                                                                                                      75 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 16
                                                                                                                                                                                                                                                                                                                                                                                  B54292 108 bp DNA GSS 20-JUN-1998 CIT-HSP-2017M1.TR CIT-HSP Homo sapiens genomic clone 2017M1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match . 46.2%; Score 67; DB 84; Length 101 Best Local Similarity 100.0%; Pred. No. 1.4e-12; Matches 67; Conservative 0; Mismatches 0; Indels
                               Indels
Pred. No. 1.3e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. 108
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="2017M1"
/clone="2017M1"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B54292 GI:2608626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HindIII"
```

RESULT AU037147

Length 528;

84;

B

Score 67.4;

46.5%;

Query Match

TITLE

```
Butkaryota, Metazoa, Chordata, Craniata, Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 144)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Barry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Simon, M. and Venter, J.C.
Simon, M. and Sequence Database for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2045D19.TF
Other_GSSs: CIT-HSP-2045D19.TF
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
Tyll Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Fax: 301 838 0208
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                     Email: midadams@figr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3-21;
Class; BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 GIGGAICCCCCGGGCCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B80294 144 bp DNA GSS 24-OCT-1998
CIT-HSP-2045D19.TR CIT-HSP Homo sapiens genomic clone 2045D19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 GEGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 14
                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 67; DB 96; Length 141;
Pred. No. 1.4e-12;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          35 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:7054558"
/db_xref="taxon:9606"
                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:7103988"
/db_xref="taxon:9606"
/clone="2172N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                          41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.2%; Soc
Best Local Similarity 100.0%; Pr
Matches 67; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B80294.1 GI:2867317
                                                                                                                                                                                                                                                                                                                                                                                                                              41
c
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 GGGGGCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Bukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                   Eukaryota; Dictyosteliida; Dictyostelium.

1 (bases 1 to 141)

Morio,T., Urushihara,H., Salto,T., Ugawa,Y., Mizuno,H., Yoshida,M.,

Morio,T., Mitzus,B.N., Pi,M., Sato,T., Takemoto,K., Yasukawa,H.,

Williams,J., Maeda,M., Takeuchi,I., Ochlai,H. and Tanaka,Y.

The Dictyostelium developmental cDNA project; generation and

analysis of expressed sequence tags from the first-finger stage of
       AU037147 141 bp mRNA EST 29-MAR-1999
AU037147 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSB532, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:44689"
/clone="SSB532"
/clone_lib="lictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGGACCTCGAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B95279 141 bp DNA GSS 26-JUN-1998 CIT-HSP-2172N2.TF CIT-HSP Homo sapiens genomic clone 2172N2, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            On Jan 19, 1998 this sequence version replaced gi:2153012. Contact: Hideko Urushihara
Institute of Biological Sciences
Institute of Tsukuba Sciences
3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoldeum cDNA project in Japan'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpulshed (1998)
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels

    141
/organism="Dictyostelium discoideum"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
46.2%; Score 67; DB 44; I
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28
                                                                                                                                                                                                                                                                                                                                                     development
DNA Res. 5 (6), 335-340 (1998)
99156227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="slug"
40 c 42 g
                                                                                                                                                  Dictyostelium discoldeum.
Dictyostelium discoldeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain-"AX4"
                                                                                                       AU037147.1 GI:3983900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B95279
B95279.1 GI:2977616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129.6GGGGCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
COMMENT
                  LOCUS
DEFINITION
                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
B95279/c
LOCUS
                                                                                  ACCESSION
                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

ద ò

ð

TITLE

Query Match

ö g ö g

BASE COUNT ORIGIN

RESULT 8 AQ013255/C LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 175)

8 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

1 Upublished (1998)

1 Upublished (1998)

1 Upublished (1998)

2 Contact: Mark Adams

2 Department of Eukaryotic Genomics

The Institute for Genomic Research

3 The Institute for Genomic Research

5 The Institute for Genomic Research

7 The Institute for Genomic Research

7 The Institute for Genomic Research

7 The Institute for Genomic Research

8 The Institute for Genomic Research

9 7 The Institute for Genomic Research

9 8 0208

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@tesgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: M13 Reverse

Class: EAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T48593 259 bp mRNA EST 02-FEB-1995 ph6f4_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6f4_19/1TV, mRNA sequence.
                        AQ041198 175 bp DNA GSS 14-JUL-1998 CIT-HSP-2335D21.TR CIT-HSP Homo sapiens genomic clone 2335D21, genomic survey sequence.
AQ041198 GI:3310469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.2%; Score 67; DB 96; L. Lilarity 100.0%; Pred. No. 1.5e-12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          دد
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2335D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50
50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "IIIDUTH
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 GGGGCC 139
                                                                                                            106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 GGGGGCC 112
                                                                                                                                                    41 GGGGGCC 35
                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10 T48593
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                       AQ041198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                  g
                                                                                                            ò
                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 169)

Adams, M. D., Rounaley, S. D., Zhao, S., Field, C. E., Bass, S., Linher, K., Sidon, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J. C.

Building (1998)
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC end search page:
Ttp://db/humgen/bac_end_search/bac_end_search.html.
Step primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                       46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                             AQ013255 169 bp DNA GSS 06-JUN-1998 CIT-HSP-2299C22.TF CIT-HSP Homo sapiens genomic clone 2299C22, genomic survey sequence.
AQ013255.1 GI:3185820
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
/clone="2045D19"
/clone_lib="CIT-HSP"
/sey="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.2%; Score 67; DB 96; Length 169; Best Local Similarity 100.0%; Pred. No. 1.5e-12; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                Query Match 46.2%; Score 67; DB 84; Length 144; Best Local Similarity 100.0%; Pred. No. 1.4e-12; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 169
/organism="Homo sapiens"
/db_xref="GDB:7154018"
/db_xref="taxon:9606"
/clone="2299222"
/clone="11b="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Other_GSSs: CIT-HSP-2299C22.TR
                                                                                                                            41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                43 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U
                                                                                                          "IIIDUHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "IIIDUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  130 GGGGGCC 136
                                                                                                                                                                                                                                                                                                                                                                                           106 GGGGGCC 112
                                                                                                                                34
```

ö

Gaps

ô

BASE COUNT ORIGIN

FEATURES

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT

FEATURES

```
/organism="Trypanosoma brucei brucei"
/strain="Clone A4"
/db_xref="Laxon:5702"
/db_xref="Laxon:5702"
/clone_lib="Bloodstream form of serodeme ILTatl.1"
/clone_lib="Bloodstream form of serodeme ILTatl.1"
/clone_lib="Bloodstream form poly (A+) enriched mRNA
/note="CDNAs were generated from poly (A+) enriched mRNA
prepared from different developmental stages of T.b. brucei
by reverse transcription followed by PCR amplification
using mini-exon and oligo(dT) primers. The CDNA generated
were utilized in RADES-PCR coupled with differential
hybridisations to identify differentially expressed mRNA
transcripts. The products which showed to be
differentially expressed were cloned DGEM -T vector.
These differentially expressed mRNA transcripts were (are
being) sequenced to generate differentially expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
Tel: 301 838 0200
Emai: and dams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: Mi3-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eurkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 386)
Adams, M.D., Rounsley, S.D., Fleld, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 GIGGAICCCCCGGGCTGCAGGAAIICGAIAICAAGTIAICGAIACCGICGACCICCAGG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B74162 386 bp DNA GSS 24-OCT-1998
CIT-HSP-2028N1.TF CIT-HSP Homo sapiens genomic clone 2028N1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 27; I
Pred. No. 1.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watch 46.2%; Score 67; DB Local Similarity 100.0%; Pred. No. 1.6 ies 67; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other GSSS: CIT-HSP-2028N1.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .386
/organism="Homo sapiens"
/db_xref="GDB:7048251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
Fax: 254 2 631 499
Email: a.osanya@cgnet.com
Seq primer: M13 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence tags.
84 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B74162.1 GI:2769849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 GGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1:
B74162/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="lbbf4_19/17v"
/clone="lbbf4_19/17v"
/clone="lbbf4_19/17v"
/clone="lbbf4_19/17v"
/clone="lbbf4_19/17v"
/clone="lbbef4_19/17v"
/clone="lbbef4_19/17v"
/clone="lbbef4_19/17v"
/clone="lbbef4"/
/clone="l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                Homo saplens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 259)
Vinogradova,T.V., Lebedev,Y.B., Kopantzev,E.P., Wagner,L.L.,
Vollk,S.V., Ermolaeva,O.D., Lavrentyeva,I., Monastyrskaya,G.S. and
Sverdlov,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 GIGGAICCCCCGGGCTGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA052885 275 bp mRNA EST 13-SEP-1996
13551 Bloodstream form of serodeme ILTatl.1 Trypanosoma brucei
brucei cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 275)
Gasnya, A., Murphy, N.B. and Pelle, R.
Trypanosoma brucei brucei cDNAs
Unpublished (1996)
On Nov 29, 1993 this sequence version replaced g1:637578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trypanosoma brucei brucei.
Trypanosoma brucei brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match

46.2%; Score 67; DB 20; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Structure and Function of Human Genes
Shemyakin Institute of Bioorganic Chemistry
16/10 Miklukho-Maklaya, Moscow, 117871, Russia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             International Livestock Research Institute
Box 30709, Nairobi, Kenya
Tel: 254 2 630 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .259
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                       Outward Alu-primed hncDNA library Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: sverd@humgen.siobc.msk.su.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA052885.1 GI:1543898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Sverdlov ED
                                                       GI:642793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 70953306529
Fax: 70953306538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 GGGGCC 122
                      T48593
T48593.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA052885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62
                                                                                                                                      human.
```

BASE COUNT ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

RESULT 11 AA052885 DEFINITION

οy 유

ö

Gaps

ò g

ô 셤

```
Eucharyota; Marazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Stass 1 to 519)

RS Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, R., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building

AL Unpublished (1997)

Other_GSSs: CIT-HSP-2022D24.TR

Contact: Mark Adams

Department of Eukaryotic Genomics

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: Mi3-21
               46 GIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCTIAICGAIACCGICGACCICGAGG 105
                                                                                                                                                                                                                 B65534 519 bp DNA GSS 21-JUN-1998 CIT-HSP-2022D24.TF CIT-HSP Homo sapiens genomic clone 2022D24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%; Score 67; DB 84; Length 51 100.0%; Pred. No. 1.7e-12; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .519
/organism="Homo sapiens"
/db_xrefe="GDB:7045730"
/db_xrefe="taxon:9606"
/clone="2022D24"
/clone_11b="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                        B65534
B65534.1 GI:2639512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity 100.
67; Conservative
                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 GGGGGC 112
                                                                                        106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGGCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A0012629
                                                                                                                          39 GGGGGCC 33
                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                               RESULT 14
B65534/c
                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                      ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1:
AQ012629
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                    g
                                                                                        ö
                                                                                                                        d
                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 462)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,

Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fex: 301 838 0200
                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ014512 462 bp DNA GSS 06-JUN-1998 CIT-HSP-2300D21.TF CIT-HSP Homo sapiens genomic clone 2300D21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
/db_xref="taxon:9606"
/clone="2028N1"
/sex="wale"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                      ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 46.2%; Score 67; DB 96; Length 462; Best Local Similarity 100.0%; Pred. No. 1.7e-12; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                46.2%; Score 67; DB 84; Length 386;
100.0%; Pred. No. 1.7e-12;
ive 0; Mismatches 0; Indels
                                                                                                                            ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115
                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:1154425"
/db_xref="taxon:9606"
/clone="2300D21"
/clone="lb="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .462
                                                                                                                          109 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ014512
AQ014512.1 GI:3184839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 c
                                                                                                                                ე
86
                                                                                                                                                                                                                     Similarity 100.067; Conservative
                                                                                                           "IIIDdIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                ๙
                                                                                                                                                                                                                                                                                                                                             106 GGGGGCC 112
                                                                                                                                                                                                                                                                                                                                                                               22 GGGGGCC 16
                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                     Best Local
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
AQ014512/c
LOCUS
                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
```

us-08-935-377-6.rst

```
Human,

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butherita; Primates; Catarrhini; Hominidae; Homo.

Butherita; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 547)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M. and Venter,J.G.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)

Contact: Mark Adams

Unpublished (1998)

Contact: Mark Adams

Tel: 301 888 0200

Fax: 301 888 0200

Fax: 301 888 0200

Fax: 301 888 0200

Email: mdadams@tigr.org

Clones are availabe from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Docation/Qualifiers
1. 547
/organism="homo sapiens"
/db_xref="GDB:7154060"
/db_xref="taxon:9606"
/clone="2299f1"
/clone="1299f1"
/clone="1299f1"
/clone=lb="CTF-HSP"
/cex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
CIT-HSP-2299F1.TR CIT-HSP Homo sapiens genomic clone 2299F1, genomic survey sequence. AQ012629 AQ012629.1 GI:3185194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154
                                                                                                              human.
                                            ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
          DEFINITION
                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                               JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

Search completed: May 29, 2000, 21:13:15 Job time: 36514 sec

셤 ò

```
X52326 piluescript
X5232 piluescript
X52327 piluescript
X52327 piluescript
LOR784 Bluescribe
LOR784 Cloning vec
U03438 Yeast integ
U03435 Yeast integ
U0344 Yeast centr
U25061 Cloning vec
U0344 Yeast centr
U25060 Cloning vec
U0345 Yeast centr
U25060 Cloning vec
U0345 Yeast centr
U25059 Cloning vec
U0347 Yeast centr
U25059 Cloning vec
U0347 Yeast centr
U25059 Cloning vec
AF01571 Mammalian
AF01239 Cloning vec
AF01239 Cloning vec
AF07239 Cloning vec
M32616 Synthetic c
X94477 Bacterial s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A44281 Sequence 9
                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARBLKSM
ARBLKSP
ARBLZKSM
ARBLZKSM
SYNBLKSW
SYNBLKSW
SYNBLKSPV
SYNDBEN66
XXU35131
PRS304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRS315
ASAJ5323
SYNPGR8V
CVU46017
AF015771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYNECOYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVU46018
AF028239
AF067646
AF072999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BSPX91477
YSCTRAM2
                                                                                                                                                                                                                                                                                                                                                                                                                                Length DB
                                                                                                                                                                                                      gb_htg11:*
gb_htg12:*
gb_htg13:*
gb_htg13:*
                                                                       em_htg3:*
em_hum5:*
gb_p13:*
gb_pr5:*
                                                                                                                                                gb_htg8:*
gb_htg9:*
gb_htg10:*
 gb_htg6:
gb_htg7:
                                    em_htg1:
em_htg2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match 1
Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \frac{1}{2} \frac{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ちゃもひてのらおくららゃととこのらおくりらずもとてつらおくのらずととてこくおんりょく ちょくしょん ちょくしょく しょしょ しょうしょ としょ こうしゅ としょう しゅうしょ しゅうしょ しゅうしょ しゅうしょ しゅうしょ しゅうしょ しゅうしょ しゅうしゅう しゅうしゅう しゅうしゅう
                                                                                                                                                                                                                                                                                                                                                                                                              Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         υυυ
                                                                                                                         May 29, 2000, 21:35:29 ; Search time 1214.87 Seconds (without alignments) 927.949 Million cell updates/sec
                                                                                                                                                                                                  US-08-935-377-7
148
1 GGCCAAAAATTGAAAAACTA......TTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                        1765538
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                   882769 seqs, 3808571567 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                            - nucleic search, using sw model
                                                                                                                                                                                                                                                                           IDENTITY_NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9b_sy:*
9b_un:*
9b_vi:*
em_fun:*
em_hum1:*
em_hum2:*
em_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_htg1:*
gb_htg2:*
gb_in1:*
                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_in2:*
em_ba1:*
em_ba2:*
em_hum3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_pr3:*
gb_ro:*
gb_sts:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_or:*
em_ov:*
em_pat:*
em_ph:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9b_om:*
9b_ov:*
9b_bat:*
9b_ph:*
9b_pl1:*
9b_pl2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_un:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                em_sts:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_pr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   em_ro:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenEmbl:*
                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                           Scoring table:
                                                                                          OM nucleic
                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                   Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                               Run on:
```

ö

Length 2958;

```
4 (bases 1 to 2958)
Lampe,D.J., Grant,T.E. and Robertson,H.M.
Factors affecting transposition of the Himarl mariner transposon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submission Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems, 11099 North Torney Pines Rd., La Jolla, CA 92037, USA 2 (bases I to 2958) Short,J.W., Fernandez,J.W., Sorge,J.A. and Huse,W.D. Short,J.W., Farnandez,J.W., Sorge,J.A. and Huse,W.D. Lambda ZAP: a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                             47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                 Query Match 46.9%; Score 69.4; DB 14; Length 2958; Best Local Similarity 87.4%; Pred. No. 1.6e-11; Aatches 76; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
88319944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="phagemid pBluescript KS(+)" 734 c 751 g 724 t
                                                                                     Score 69.4; DB 14;
Pred. No. 1.6e-11;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 2958
/organism="synthetic construct"
/db_xref="taxon:32630"
1. 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 (bases 1 to 2958)
Alting-Mees,M.A. and Short,J.M.
Bluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics 149 (1), 179-187 (1998)
98250682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 GGGGGGCCTAACTAACTATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
  731
                                                                                     Query Match

Best Local Similarity 87.4%;
Matches 76; Conservative (
  754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thomas, E.A.
    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          749
  708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                         RESULT
ARBLKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                유
                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                             unidentified.
unidentified
unidentified
unclassified.
uncl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas, E.A. Submission Submission Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems, 11099 North Torney Pines Rd., La Jolla, CA 92037, USA C (Asses 1 to 2958) Short, J.W., Fernandez, J.W., Sorge, J.A. and Huse, W.D. Lambda ZAP: a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARBLKSM 2958 bp DNA circular SYN 10-MAY-1995 pBluescript KS(-) vector DNA, phagemid excised from lambda ZAP. X52326 X52361 GI:58064 artificial sequence; cloning vector; expression vector; synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.2%; Score 69.8; DB 5; Length 2 ilarity 79.0%; Pred. No. 9.4e-12; Conservative 0; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .2958
/organism="synthetic construct"
/organism="taxon:32630"
1. .2958
/note="phagemid pBluescript KS(-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .259
/organism="unidentified"
/db_xref="taxon:32644"
/clone_lib="MousE GENOMIC LIBRARY"
/clone="M3.2" 63 g 69 t 2
                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 2958)
Alting-mees/m.h. and Short,J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
                                                                                   A44281 259 bp DNA
Sequence 9 from Patent WO9511300.
A44281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         artificial sequence.
1 (bases 1 to 2958)
                                                                                                                                                                           A44281.1 GI:2299115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
                                                                                                           LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                              RESULT
A44281/c
                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
ARBLKSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
```

0; Gaps

```
KEYWORDS
CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNBLKSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                       747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                       BASE COUNT
ORIGIN
TITLE
JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
SYNBLKSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                        Direct Submission
Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
2 (bases 1 to 2961)
Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacterlophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 2961)
Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacterlophage lambda expression vector with in vivo
                                                                                                        cloning vector; expression vector; vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems.
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cloning vector; expression vector; vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIATCAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               685 TAGTGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARBL2KSP 2961 bp DNA circular SYN 10-MAY-1995
pBluescript II KS(+) vector DNA, phagemid excised from lambda
ZAPII.
                ARBL2KSM 2961 bp DNA circular SYN 10-MAY-1995 pBluescript II KS(-) vector DNA, phagemid excised from lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.9%; Score 69.4; DB 14; Length 2961; Best Local Similarity 87.4%; Pred. No. 1.6e-11; Matches 76; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualiflers
1. .2961
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .2961
/note="phagemid pBluescriptII KS(-)"
a 758 c 735 g 762 t
                                                                                                                                                                                                                                                                                                  excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
88319944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
88319944
                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 2961)
Alting-Mees,M.A. and Short,J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 2961)
Alting-Mees, M.A. and Short, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 2961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             artificial sequence;
synthetic construct.
synthetic construct
                                                                                  X52329.1 GI:58060
artificial sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              artificial sequence.
1 (bases 1 to 2961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X52327
X52327.1 GI:58061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thomas, E.A.
                                                                                                                                                                                           Thomas, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                  DEFINITION
                                                                                                                                         ORGANISM
                                                                                                                                                                                         AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                  ACCESSION
                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARBL2KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lac2 region is on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #journal Gene (1987) in press
#citation Sequence data from StrataGene
#comment sequence correction according to Stratagene COMMENT
Obtained from StrataGene on floppy disc.
Revised 02-FEB-1987 by F. Pfeiffer:
1409/10 'AT' to 'TA' to match revised sequence of PBR322
Revised 4 'MAR-1987 to match sequence of pUC19 on request
of Stratagene
Polylinker region revised 03-APR-1987 according to Stratagene
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1991)
Hase data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. BlueScribe KS Minus - Cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This vector contains the fl origin so that the minus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                                                                                                                                                                                                             47 IGGIGGATCCCCCGGGCTGCAGGAATICGATATCAAGCTTAICGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                               Length 2961;
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENTRY BLUEKSM
TITLE BlueScribe KS Minus - Cloning vector
DATE 28-JAN-1987
                                                                                                                                                                                            /note="phagemid pBluescriptII KS(+)"
738 c 755 g 721 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                circular SYN
                                                                                                                                                                                                                                                                                                               Score 69.4; DB 14;
Pred. No. 1.6e-11;
0; Mismatches 11;
                                                                                                1. .2961
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .2961
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bluescribe KS Minus cloning vector.
L08784
L08784.1 GI:310728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence 02-FEB-1987
#sequence 04-MAR-1987
#sequence 03-APR-1987
ACCESION VB0077
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Obtained from VecBase 3.0
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 87.4%;
Matches 76; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2964 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               artificial sequence.
1 (bases 1 to 2964)
Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic construct
synthetic construct
```

```
The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lacz region is on the complementary strand.
                                                                                                                                                                                                                                                                                  #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kpni-Drail-Apal-Xhoi-Sali-Clai-Hindili-ECORV-ECORI-PstI-Smail-BamHI-Spei-Xbai-Noti-Xmaili-BstXi-Sacii-Saci SELECTION #resistance Ap #indicator beta-galactosidase #indicator beta-galactosidase summARY = llueKSp #length 2964 #checksum 690.

1. 2964
                                                                                                                                                                                                                                                                                                                     #journal Gene (1987) in press
#citation Sequence data from StrataGene
#comment sequence correction according to Stratagene COMMENT
Obtained from StrataGene on floppy disc.

Revised 0.2-FEB-1987 by F. Pfelffer:
1409/10 'AT' to 'TA' to match revised sequence of PBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polylinker region revised 03-APR-1987 according to Stratagene
These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. BlueScribe KS Plus - Cloning vector ENTRY BLUEKSP TITLE BlueScribe KS Plus - Cloning vector OPATE 28-JAN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3, VecSource(3):bGalKS, GenBank(50):PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This vector contains the fl origin so that the plus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             643 start of T7-RNA synthesis 774 (c) start of T3-RNA synthesis 1976-2764 789-1 (c) Ap-R; b-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              653-760 108- 1 (c) BlueKS-polylinker 772-791 20- 1 (c) T3 promoter 772-791 23- 1 (c) T3 promoter 1035-1031 237- 1 (c) pUC19 conflict (cfl) and Mutations (mut): none FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108- 1 (c) BlueKS-Polylinker 20- 1 (c) T3 promoter 448-2617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 795-2964 448-2617 puclyc Conflict (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VecBase(3):BlueKSm, VecBase(3):BlueSKp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5943-5488 (c) phage f1
449-285 (c) pUC19
1-20 T7 promo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         residue source
3- 458 5943-5488 (c) phage fl
460- 624 236- 400 pUC19c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Features of BlueKSp (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Features of BlueKSp (2964 bp)
                                                                                                                                 #sequence 02-FEB-1987
#sequence 04-MAR-1987
#sequence 03-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VecBase(3):BlueM13p
                                                                                                                                                                                                                          artificial
                                                                                                                                                                                                    ACCESSION VB0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYLINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KpnI-DraiI-ApaI-XhoI-SalI-ClaI-HindIII-EcoRV-EcoRI-PstI-
SmaI-BamHI-SpeI-XbaI-NotI-XmaIII-BstXI-SacII-SacI SELECTION
                                                                         VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3, VecSource(3):bGalKS, GenBank(50):PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 46.9%; Score 69.4; DB 14; Length 2964; Best Local Similarity 87.4%; Pred. No. 1.6e-11; Matches 76; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #checksum 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  643 start of T7-RNA synthesis
774 (c) start of T3-RNA synthesis
1976-2764 789-1 (c) Ap-R; b-lactamase
                                                                                                                                                                                                                                                       108 1 (c) Blueks-polylinker
20 1 (c) 13 promoter
448-2617 nnon-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T7 promoter
BlueKS-polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653-760 108- 1 (c) BlueKS-polylink(772-791 20- 1 (c) BlueKS-polylink(795-1031 237- 1 (c) pUG19 1032-2964 2686-754 (ć) pUG19 CONÍLICT (cfl) and Mutations (mut): none FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular SYN
                                                                                                                                                                                                                                                                                                                                                           Conflict (cfl) and Mutations (mut): none
                                                                                                                                            VecBase(3):BlueKSp, VecBase(3):BlueSKm

    1. .2964
    /organism="synthetic construct"

                                                                                                                                                                                                                                                                                                                                                                                                                                                phage fl
puc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  765 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNBLKSPV 2964 bp DNA circ
BlueScribe KS Plus cloning vector.
L08785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #resistance Ap
#indicator beta-galactosidase
MARY BlueKSm #length 2964
                                                                                                                                                                                                                                                                                                                                                                                                        Features of BlueKSm (2964 bp)
                                                                                                                                                                                        Features of BlueKSm (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:32630"
756 c 735 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GGGGGGCCTAACTAACTATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 égégégécegeracceaecririerr 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           5488-5943
449- 285 (C)
                                                                                                                                                                                                 3-458 5488-5943
460-624 236-400
626-645 1-20
653-760 108-1 (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obtained from VecBase 3.0 Unpublished (1991)
                          parent
VecBase(3):BlueM13m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic construct DNA synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         artificial sequence.
1 (bases 1 to 2964)
Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L08785.1 GI:310729
                                                                                                                                                                                                                                                                                                                                                                                                                                residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYLINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                        PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNBLKSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                á
```

```
862
   /product="beta-lactamase"
              /protein_id="BAA12825.1"
/db_xref="G1:1345435"
                                                                                                                                                                                                                                                                                                                              107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                             GGGGGGCCCGGTACCCAGCTTTTGTT 37
                                                                                                                                        790 9
                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 160 (1), 63-67 (1995)
95354958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                    46.9%;
ilarity 87.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         4144 bp
                                                                                                                           EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EIGASLIKHW"
                                                                                                                                          800 c
                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        XXU35131
                                                                                                                                          854
                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                          COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
XXU35131
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                        BASE CO
ORIGIN
                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSHIQRETSCSRPRLNSNMDADLYGYKWARDNVGGSGATIYRLY
GKPDAFLEFEKHGKGSVANDVTDEMVRLNWFLFEMFLPTIFTPDDAWLLTAIP
GKTAFQVLEEYPDSGBNIVADLAVFTRRLHSIPVCNCPFNSDRYFRLAGAGSRNNNGL
VDASDFDDERNGWPYEVBQVWKRMHKLLPFSPDSVYTHGDFSLDNLIFDEGKLIGGLUVG
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                              A circular SYN 06-FEB-1999
for aminoglycoside 3'-phosphotransferase,
                                                                                                                                                                                                                                                                   SINPBEN66 3306 bp DNA circular SYN 06-FEB-1999
Cioning vector pageN66 DNA for aminoglycoside 3'-phosphotransfera;
beta-lactamase, complete cds.
SION D88525
N D85525.1 GI:1345433
DS plasmid; aminoglycoside 3'-phosphotransferase; beta-lactamase.
Cloning vector pageN66 (lab_host:E.coli) plasmid:pBEN66 DNA.
TSM Cloning vector pageN66
artificial sequence; vectors.
S Yamamoto,Y.
S Yamamoto,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVGIADRYQDLAILWNCLGEFSPSLQKRLFQKYGIDNPDMNKLQFHLMLDEFF" complement(2209. .3069)
                                                                                                                                                     TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                     'note-"derived from Tn903; kanamycin resistance gene"
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-MAY-1996) to the DDBJ/EMBL/GenBank databases. Yoshihiro Yamamotto, Hyogo College of Medicine, Department of Genetics; Mukogawa-cho 1-1, Nishinomiya, Hyogo 663, Japan (Tel:0798-45-6587, Fax:0798-40-7639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
/product="aminoglycoside 3'-phosphotransferase"
/db_xref="GI:1345434"
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto, Y. and Furuyama, J. One-step disruption by circular DNA in Escherichia coli Unpublished (1996)
                                                                                            Length 2964;
                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 3306
/organism="cloning vector pBEN66"
/plasmid="pBEN66"
/db_xref="taxon:47800"
/lab_host="E.col1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="amipicillin resistance gene"
                                                                                          Score 69.4; DB 14;
Pred. No. 1.6e-11;
0; Mismatches 11;
 construct"
                              u
                              723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(2209. .3069)
/organism="synthetic c
/db_xref="taxon:32630"
736 c 755 g
                                                                                                                                                                                                                    107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                     19. .36
/note="T3 promoter"
260. .1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="kan"
260. .1075
/gene="kan"
                                                                                          46.9%;
llarity 87.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /citation=[2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="amp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (sites)
                                ಥ
                                                                                          Query Match
Best Local Simi
Matches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                            SYNPBEN66/c
LOCUS
                                                                                                                                                                                                                                                                                                                                             DEFINITION
                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                        47
                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                     g
                                                                                                                                                                                                                                                   g
G
                                                                                                                                                                                                                      ð
                                                                                                                                                          ö
```

```
/function="ampicillin resistance"
/product="beta-lactamase"
/protein_id="AAC53618.1"
/db_xref="151:984908"
/translation="ASIGHERVALIPFFAAFCLPVFAHPETLVKVKDAEDOLGARVGY
IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGOEOLGRRIHYSQNDLVE
XSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGFKELTAFLHNMGDHVTRL
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4144)
Hengen, P.N.
Direct Submission
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
Location/Qualifiers
1. 4144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   omega elements
                                                                                                                                                                                                                                                                                                                                                   TGGTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                         123 TAGTGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACGGTGGA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-1995
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                        Length 3306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning vector pBSL159.
Cloning vector pBSL159
artificial sequence; vectors.
[ Dases 1 to 414, ]
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omegfor Escherichia coll vector construction and in vitro deletion,insertion mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
/product="chloramphenicol acetyltransferase"
/protein_id="AAC53619.1"
/db_xref="GI:984909"
                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pBSL159 cloning vector, complete sequence. U35131
U35131.1 GI:984907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(3704. .4144,1. .219))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Cloning vector pBSL159"
/plasmid="pBSL159"
/db_xref="taxon:42704"
complement(1129. .1989)
/EC_number="3.5.2.6"
/codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYN
                                                                                                                                                                                                                                                  Score 69.4; DB 14;
Pred. No. 1.6e-11;
O; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     circular
```

omega elements

```
/translation="MIEDDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAGGR
PVLFYKTDLSGALNELQDEAARLSWLATGYPCAAVLDVYPEAGRDWLLGEVPGQDL
LESHLAAPERVSIMADAMRILHTLDPATCFFDHQAKHRIERAATRWEAGLVDQDDLDE
EHQGLAPAELFARLKARMPOGEDLVYTHGDACLPNINVENGRFSGFIDGGRLGVADRY
QDIALATRDTAELGGEWADDFLVYTGIAAPDSQRIAFYRLLDEFF"
/CC_number="315.2.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
/function="ampicillin resistance"
/product="beta-lactamase"
/protein_id="AAC53630.1"
/db_xref="G1:984925"
/translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGOEGLGRRIHYSONDLVE
SPYTEKHLTDGMYVELCSAAITMSDNTAANLLTITGGGREITAFBHINGDHYTRL
DRWEPELNELNELPUDERDTIMPWAMTILKKLLTGELLILASROGLIDMWEAVNAGPL
IRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYITGSQATMDERNRQIA
                                                                                                                                                                                                         Direct Submission
Direct Submission
Submitted (31-Aug-1995) Paul N. Hengen, Laboratory of Mathematical Submitted (31-Aug-1995) Paul N. Hengen, Laboratory of Mathematical Biology, National Cancer Institute, Frederick, MD 21702-1201, USA Location/Qualifiers
1. .4289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRS306 4373 bp DNA circular SYN 14-SEP-19
Yeast integrative vector pRS306 with URA3 marker, complete
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.4; DB 14; Length 4289; Pred. No. 1.7e-11;
cloning vector pBSL97.
Cloning vector pBSL97.
Cloning vector pBSL97

artificial sequence; vectors.
I (bases 1 to 4289)
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omegfor Escherichia coli vector construction and in vitro deletion/insertion mutagenesis
Gene 160 (1), 63-67 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="neomycin phosphotransferase"
/protein_id="AAC53629.1"
/db_xref="GI:984924"
                                                                                                                                                                                                                                                                                                                     /organism="cloning vector pBSL97"
/plasmid="pBSL97"
/db_xref="taxon:427"
complement(804. .1598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 GGGGGGCCTAACTAACTATTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning vector pRS306.
Cloning vector pRS306
artificial sequence; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1111
                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 87.4%;
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EIGASLIKHW"
1157 C
                                                                                                                                                                                               (bases 1 to 4289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:416307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         003438.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                   AUTHORS
TITLE
                                                                                                                                                          JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                  AUTHORS
                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
PRS306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
         /translation="MekkItgytyudisQWHRKEHFEAFOSVAQCTYNQTVQLDITAF
LKTYKKNKHKFYPAFIHILARLANAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETF
SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFTMGKXYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cloning vector pRS304.
Cloning vector pRS304
artificial sequence; vectors.
1 (Dases 1 to 4267)
Sikorski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae
Genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                     47 IGGIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCITATCGAIACCGICGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-1995
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRS304 4267 bp DNA circular SYN 14-SEP-1995
Yeast integrative vector pRS304 with TRP1 marker, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4267;
                                                                                                                                                                                 Length 4144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XXU35136 4289 bp DNA circular SYN
Plasmid pBSL97 cloning vector, complete sequence.
U35136.1 GI:984923
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Cloning vector pRS304"
/db_xref="taxon:31827"
965 c 1092 g 1082 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 69.4; DB 14;
Pred. No. 1.7e-11;
0; Mismatches 11;
                                                                                                                                                                               Score 69.4; DB 14;
Pred. No. 1.7e-11;
0; Mismatches 11;
                                                                                                        1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2784 GGGGGGCCCGGTACCCAGCTTTGTT 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GGGGGGCCTAACTAACTAATTTGTT 133
                                                                                                                                                                                                                                                                                                                                  107 GGGGGGCCTAACTAACTAATTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84132, USA
Location/Qualifiers
                                                                                                          959 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 46.9%;
Best Local Similarity 87.4%;
Matches 76; Conservative (
                                                                                                                                                                                 ch 46.9%;
1 Similarity 87.4%;
76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 4267)
Stillman, D.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U03436
U03436.1 GI:416305
                                                                                                            υ
                                                                                                            1009
                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ๗
                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89276910
                                                                                                            1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      City,
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
XXU35136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                           10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
PRS304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                   셤
```

ö

Gaps

ö

11; Indels

997

÷.

```
AJ005329.1 GI:4028990
gltS gene; glutamate permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . ; . ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1040
                                                       ASAJ5326/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
ASAJ5329
                                                                                                                                                                                      ORGANISM
                                                                                                       DEFINITION
                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                 2165
                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                          TITLE
                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                    Direct Submission
Submitted (10-NoV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132, USA
Location/Qualifiers
1. 4373
/organism="Cloning vector pRS306"
/db_xref="taxon:31829"
1181 a 987 c 1106 g 1099 t
                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning vector pRS303.
Cloning vector pRS303
artificial sequence; vectors.
1 (bases 1 to 4443)
Sikorski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae genetics 122 (1), 19-27 (1989)
1 (bases 1 to 4373)
Sikorski,R.S. and Hieter,P.
A system of Shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                     2105 TAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 2164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-SEP-1995
complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 46.9%; Score 69.4; DB 14; Length 4443; 1 Similarity 87.4%; Pred. No. 1.7e-11; 76; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                          Length 4373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRS303 4443 bp DNA circular SYN
Yeast integrative vector pRS303 with HIS3 marker,
sequence.
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                          Score 69.4; DB 14;
Pred. No. 1.7e-11;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 .4443
/organism="Cloning vector pRS303"
/db_xref="taxon:31826"
a 1048 c 1109 g 1137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2085 GGGGGGCCCGGTACCCAGCTTTTGTT 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GGGGGGCCTAACTAACTATTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              City, UT 84132, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          Match 46.9%;
Local Similarity 87.4%;
les 76; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 4443)
Stillman, D.J.
Direct Submission
                                                                                         2 (bases 1 to 4373)
Stillman, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U03435.1 GI:416304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                       source
                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
 REFERENCE
AUTHORS
TITLE
                                                                           MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                            Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    윱
                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                         ä
```

```
/codon_start=1
/transl_table=11
/product='glutamate permease"
/product='glutamate permease"
/product='glutamate permease"
/product='glutamate permease"
/product='glutamate permease"
/product='glutamate | permease | perme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AWACAȚEGULGGPVAROLILIKGNKSWVPGPPSRSTVSISLISNSCSPGDPLV
LERPPRWASSNSPYSESYTARILVKHSTPNCI-DODGWPTAFERPDVGRITSLLI
EITALIAICHTVGRAFELARILAGTAFELPTPVCVLFVGVILSNGLSINGFYRVERAVS
VLGNVSLSLFLAMALMGLKLWELASLALPMLAILVVQTIFMALYAIFVTWRMMGRNYD
AAVLAAGHCGFGLGATPTAIANMQAITERFGPSHWAFLVVPMVGAFFIDIVNALVIKL
YLMLDIFFG"
1231 g 1234 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (03-APR-1998) Gal J., Institute for Biotechnology, Bay
Zoltan Foundation for Applied Research, Szeged, Derkovits fasor
6726, HUNGARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASAJ5329 4670 bp DNA circular SXN 08-FEB-1999 pGAII(-) KS positive selection cloning vector gltS gene. AJ005329
                                                                                                                                                                                                                                                                                            ASAJ5326 4670 bp DNA circular SYN 08-FEB-1999 pGANI(+) KS positive selection cloning vector gltS gene. AJ005326 AJ005326.1 GI:4028984 gltS gene; glutamate permease. Synthetic construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A positive selection cloning system based on the gltS gene of Escherichia coli
Anal. Blochem. 266 (2), 235-238 (1999)
99107575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Simoncsits, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pongor, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
46.9%; Score 69.4; DB 14;
Best Local Similarity 87.4%; Pred. No. 1.7e-11;
Matches 76; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construct"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 4670)
Gal,J., Szekeres,S., Schnell,R.,
Kalman,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .4670
/organism="synthetic co/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1442 GGGGGGCCCGGTACCCAGCTTTGTT 1416
107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 852. .2231
/gene="gltS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852. .2231
/gene="glts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       artificial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
```

```
complement(1150..2529)
gene="gits"
/codon_start=1
/cransl_table=11
/transl_table=11
/transl_table=11
/product="gittamate_permease"
/product="gittamate_permease"
/product=10146-70A06476.1"
/db_xref="Git(02899)
/db_xref="Git(02899)
/translation="MFHLDTLATLVAATLTLLLGRKLVHSVSFLKKYTIPEPVAGGLL
/translation="MFHLDTLATLVAATLTLLLGRKLVHSVSFLKKYTIPEPVAGGLL
/translation="MFHLDTLATLVAATLTLLLGRKLVHSVSFLKKYTIPEPVAGGLL
/translation="MFHLDTLATLVAATLTLLGRKLVHSVSFLKKYTIPEPVAGGLL
/translation="MRHLDTLATLVKKSWYPGPPSRSTVSFLIETTLVVV
GLLVWQNAIGIGGASLLGGPARQLTLKGNKSWYPGPPSRSTVSISLISNSCSPGDPLV
AMACATFGIVLGGPARQLLGATFELPTFVCVLFVGVILSNGLSINGFYRPERAVS
YLGRVSLSLFLAMALMGLKJMELASIALPMIALIUTUTKLAAGHGGFCLGATPTAIANMQAITERFGPSHMAFLVVPWVGAFFIDIVNALVIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
synthetic construct.
synthetic construct
artificial sequence.
1 (bases I to 4670)
Gal,J.
Direct Submission
Submitted (03-APR-1998) Gal J., Institute for Biotechnology, Bay 201tan Foundation for Applied Research, Szeged, Derkovits fasor 2., 6726, HUNGARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 TGGTGGATCCCCCGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                         Gal., Szekeres, S., Schnell, R., Pongor, S., Simoncsits, A. and Gal., Szekeres, S., Schnell, R., Pongor, S., Simoncsits, A. and Kalman, M. A positive selection cloning system based on the gltS gene of Escherichia coli Bischem. 266 (2), 235-238 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.4%; Pred. No. 1.7e-11;
Matches 76; Conservative 0; Mismatches 11; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                         1. 4670.
/organism-"synthetic construct"
/db_xref="taxon:32630"
complement(1150. .2529)
/gene="gits"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1076 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1939 GGGGGGCCCGGTACCCAGCTTTTGTT 1965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 GGGGGGCCTAACTAACTATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1145 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: May 29, 2000, 21:35:34
Job time: 36866 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLMLPIFAG"
1251 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
  SOURCE
ORGANISM
                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                   MEDLINE
FEATURES
                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

ţ.

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

- nucleic search, using sw model OM nucleic

May 29, 2000, 21:58:21 ; Search time 1446.77 Seconds (without alignments) 25:594 Million cell updates/sec Run on:

US-08-935-377-7

Title:

148 1 GGCCAAAAATTGAAAAACTA......TTGTTTTTGTGGGCCCGGCC 148 Perfect score: Scoring table: Sequence:

311585 segs, 125096042 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

623170

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

COLORADO

WO9802563-A1

SUMMARIES		Description	Maize fluory2 g	Mouse azoospermia	Nucleotide analogu	Human endogenous r	Plasmid priphar (r	Human endogenous r	Polynucleotide seq	₽	pG+1		Plasmid pG+host5 c	Plasmid pG+host6 c	Swedish-FAD APP ta	London-FAD APP tar	Swedish/London-FAD	Swedish-FAD APP713		Ė	E. coli biotin DNA	DE19731274 Seq ID	DE19731274 Seq ID	DE19731274 Seg ID	DE19731274 Seq ID		Human endogenous r		Stealth virus plas	ld pAT-1	$\sim$	otide se		Candida CaRhol gen
SUMIN		£	V09028	087664	T04866	T75006	T43794	T75005	X20513	V31294	048463	T39485	048464	048465	X24730	X24731	X24732	X24733	V68808	026664	X02800	X02814	X02815	X02812	X02813	V57377	T75010	V10190	V12003	T04575	V22271	V69740	T49876	T92702
		В		ч	-	-	-	-	ч	ч	н	н	-	Н	Н			٦	1	Ч	-		-		-		Н	Н	-	~	Н	7	Н	
		Length	0529	259	501	1091	5356	1122	651	752	3792	4226	5234	6722	12814	15692	15692	15701	545	2640	84	3465	3481	3794	3810	6596	545	685	685	4164	4164	4164	5178	3198
,	Query			7.		ė	'n.	ь.	•	45.5	ď.	ď.	•	ď.	S.	S.	•	ů.	'n	4	•	₩.	س	•	ω.	43.9	щ	ς.	ς.	。	ö	٠.		39.3
		Score	÷.	•	ď.	æ	9		67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4	67.4			65	65	65	65	65	65	9	ö	'n	o,	o,	o,	œ.	58.2
	Result	No.	c 1		m		0		7	დ ს		10		c 12	13	14	15	16	c 17		19		c 21				c 52	56	27	28	29	30	31	32

	34	56.4	38.1		н		from muta
	35	4.4	38.1	1949	٦,		sedneuc
O I	9 5		37.8		٦,		otin DNA
ပ	\ o		0.70		٦.	reast	checkpoint c
ر	9 G	2 10	9.0		٦.	V64254 V6	S varian
	40		37.8			Plasmid	DPK13/14 D
	41		37.8		ı –	Plasmid	PPK5/6 DNA
	42		37.8		Н	Plasmid	DPK9/10 DN
	43		37.8		-	Plasmid	DPK7/8 DNA
	44		36.8	-	Н	DNA segu	ce of ex
	45		36.5		-		Murf ORF
						ALIGNMENTS	
RES	RESULT 1						
î A	V09028	8 standard;	ard;	DNA; 10	10529	BP.	
AC	V09028;	8,					
ξĠ	20-20	20-JUL-1998	(first	(first entry	<u>ک</u>		
DE	Malze	rluory	z gen	e (112)			
X	Flour	y2; f12	gene	; alpha	26	Floury2; fl2 gene; alpha-zein; signal peptide; transgenic plant;	
¥ .	seed;	essent	18. a	mino ac	ģ	animai reed; maize; rice; wheat;	
₹ C	parley;	bariey; millet;		sorgnum; as	g		
3 6	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	αys.	Ĺ	4000	ξ	1,000 tion (0.101) files	
T E	misc	misc feature		760	3	Sinite	
E				*tag=	æ		
F			. `	note= "	vec	/note= "vector-derived sequence"	
FT	promoter	ter	. ~	7613824	24		
FI			`	6	Д		
FT			. `		Cla	"Claim 14"	
FT	CDS		m		613		
FT			`		U		
FT	s1g_p	sig_peptide	m '		3887		
E-		•	`	L	ָ ק		
FF	matp	mat_peptide	m`	7.	610		
1 20	C C C C C	WO0802563-81	`	/* Lag=	D)		

Cereal plants containing trans-gene expressing fusion that includes signal peptide of the f12 maize gene - and protein having high content of essential amino acids, producing feeds of improved nutritional value

Tutritional value

Claim 14; F1g 1A.H; 37pp; English

Claim 14; F1g 1A.H; 37pp; English

This is the nuclectide sequence of a clone of the fluory2 (f12)

Gene of maize. It codes for a 24 kDa alpha-zein protein (see W23977). that includes a 21-amino acid signal peptide (see W23976)

W150 frargets the alpha-zein to the lumen of the rough endoplasmic reticulum. A claimed cereal plant contains a transgene comprising a first polynucleotide that encodes the f12 signal peptide and a second polynucleotide that encodes an agronomically high-value protein. Also new are seeds produced by the plants, the transgene treath also includes the f12 promoter. The second polynucleotide preferably encodes a protein that has a high content of Met, Lys, Trp and/or Thr so that feeds from transformed maize, wheat, rice, barley, millet or sorghum will have increased contents of these essential amino acids in their seeds (all Ë 2262 G; 2484 C; 22-JAN-1998. 11-JUL-1997; U11723. 17-JUL-1996; US-021833. (PION-) PIONEER HI-BRED INT INC. (UYAR-) UNIV ARIZONA STATE. Beach L, Coleman CE, Larkins BA; WPI: 98-110609/10. P-PSDB; WZ3977. 2845 A; 10529 BP; claimed)

Score 71.8; DB 1; Length 10529; Pred. No. 9.8e-16;

48.58; 76.58;

Query Match Best Local Similarity

61

g ŏ

à

Matches

Mus sp.

```
Reeve MA, Robinson PS;

Reeve MA, Robinson PS;

Reeve MA, Robinson PS;

Rever MA, Robinson PS;

Rever MA, Robinson PS;

Rever Majoration of residual fluorescence labelled nucleotide analogues - to prevent migration in electrophoretic sequencing gel and interference with base calling of DNA chains.

Example; Fig 1; 18pp; English.

C The invention concerns the modification of redisual fluorescence of the invention concerns the modification in electrophoretic labelled nt analogues to prevent migration in electrophoretic condification involves the use of a phosphatase enzyme to remove at modification involves the use of a phosphatase enzyme to remove at last one 5'-phosphate gp. The nts were prepared using ABI Amplitage conditions in The remplate used was 1 microg. of M13 mp8. The primer was M13 Universal primer. Samples were recovered. Some were conjected to calf intestinal alkaline phosphatase digestion. This includes 704866. To 4867 was a control nt. Which was not treated with a labiline phosphatase. The example shows that alkaline phosphatase calling with the ABI analysis software.

C treatment causes removal of the dye-terminator artefacts and allows for a courate base calling with the ABI analysis software.

So Sequence 501 BP; 98 A; 136 C; 140 G; 121 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T Endogenous human tumour-associated retroviral element, B18Ag1 - used for the prognosis, diagnosis and monitoring of human cancers, especially breast cancer as claim 10; Page 31-32; 74pp; English.

C claim 10; Page 31-32; 74pp; English.

C Human endogenous retroviral sequences 10, 11-29, 3, 6, 12, 13, 14

Human endogenous retroviral sequences tumour-associated retroviral element of 11-22 (775003-10) were obtd. by screening human genomic and 11-22 (775003-10) were obtd. These non-contiguous sequences in 11-22, 14, B18Ag-1, 13, 12, 10, 3, 11-29, 6 in the retrovirus genome (see also 775001). B18Ag1 and the other retroviral sequences can be used in genetic vaccines and for the prognosis, diagnosis and monitoring of human breast cancer.

C sequence 1091 BP; 79 A; 350 C; 97 G; 248 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 CGCNCTAGAACTAGATGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 CGCGGCCGCCATGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-0CT-1997 (first entry)
Human endogenous retroviral sequence 6.
Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 68.6; DB 1;
Pred. No. 6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 69.8; DB 1;
Pred. No. 1.7e-15;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GTCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 GTCGACCTCGAGGGGGCCCGGTACCCAGCTTTTGTT 141
/*tag= a
/note= "std. IUPAC codes used"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T75006 standard; DNA; 1091 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.2%;
81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUL-1997.
10-JAN-1997; U00398.
10-JAN-1996; US-587329.
(CORI-) CORIXA CORP.
Frudakis IN. Smith JM;
WPI; 97-384982/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 81.6
Matches 80; Conservative
                                                                                      07-MAR-1994; EP-301636.
                                                                                                                           (AMSH ) AMERSHAM INT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                  14-SEP-1995.
07-MAR-1995; G00490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human retrovirus WO9725431-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A mouse gene partial sequence (087664) showing homology to the human azoospermia factor (AZF) YRWM gene was obtd. from mouse genomic phage clone M3.2 isolated from a genomic library screened with MYK (YRRM1) cDNA (Q87655). M3.2, cloned in Lambda 2001, was mapped to the short arm of the mouse Y-chromosome. A full cDNA sequence (Q87665) was also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            calf intestinal alkaline phosphatase.
                                                                                      774 GECTABABATTECATGAGGTCCACCGGGGGGGGCGGCTCTAGABCTAGTGGATCCCCCG 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 IATIGCACGCGCCGCCATGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTAT 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid encoding the human azoospermia factor, and probes and antibodies specific for the sequence and encoded polypeptide - may be used in the clinical diagnosis of male infertility Disclosure; Fig 5; 40pp; English.
                                                  GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGGTGGATCCCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/note= "base n at position 174 is not identified
in the specification"
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag- b
/note- "base n at position 197 is not identified
in the specification"
                                                                                                                               GGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sharkey AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69.8; DB 1; Length 25
Pred. No. 1.4e-15;
0; Mismatches 22; Indels
         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATACCGTCGACCTCGAGGGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                      06-MAR-1996 (first entry)
Mouse azoospermia factor (AZF) gene partial clone M3.2.
Azoospermia factor; AZF; male infertility; YRRM gene;
Y-chromosome; RNA recognition motif; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-0CT-1994; G02344.
22-0CT-1993; GB-021857.
07-JUL-1994; GB-013760.
Changley AC, Cooke HJ, Hargreave TB, Kun M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-1996 (first entry)
Nucleotide analogue treated with calf intestin
Nucleotide analogue; alkaline phosphatase; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 G;
         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .501
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T04866 standard; DNA; 501 BP.
T04866;
28-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 47.2%;
1 Similarity 79.0%;
83; Conservative
                                                                                                                                                                                                                                                      RESULT 2
087664/c
ID 087664 standard; DNA; 259 BP.
AC 087664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 A;
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chandley AC, Cool
WPI; 95-170221/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9511300-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
```

ö

ö

- nseq

83

셤 ö RESULT 104866 ID 1C AC TC DT 22 DD NY KW NY CS SY FH KY

)

Matches

ô g ò g RESULT

```
743 TCCACTTGGAGTGGGTTGGGGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGA 684
                                                                                                                                                                                                                                                                                                                                                                              17-JUL-1997.
10-JAN-1995; U00398.
10-JAN-1996; US-587329.
(CORI-) CORIXA CORP.
Frudakis TN. Smith JM;
WPI: 97-384982/35.
Endogenous human tumour-associated retroviral element, B18Ag1 - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTAGATCTATTTATTGCACGCGGCCGCCATGGTGGATCCCCCGGGCTGCAGGAATTCGAT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 CTAAAATCCT.CCATTTCTTGGTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGAT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis claim 1: Page 257: 1150pp; English.
X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide sequence from the genome of Treponema pallidum. Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        especially breast cancer claim monitoring of human cancers, especially breast cancer claim 10; Page 30-31; 74pp; English.

Claim 10; Page 30-31; 74pp; English.

Human endogenous retroviral sequences 10, 11-29, 3, 6, 12, 13, 14 and 11-22 (775003-10) were obtd. by screening human genomic libraries using human breast tumour-associated retroviral element 118 and 11-22, 14, 1818Ag-1, 13, 12, 10, 3, 11-29, 6 in the retroviral sequences can be used in genetic vaccines and for the proposals, diagnosis and monitoring of human breast cancer. Sequence 1122 Bp; 260 A; 316 C; 185 G; 279 T;
                                                                                                                                                                                                                                                                      numman enaogenous retroviral sequence 3.
Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine; ss.
Human retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 45.7%; Score 67.6; DB 1; Length 1122; Best Local Similarity 80.6%; Pred. No. 1.4e-14; Matches 79; Conservative 0; Mismatches 19; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 ATCAAGCITATCGAIACCGICGACCTCGAGGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCC 42
                                               92 TACCGTCGACCTCGAGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
de sequence from the
                                                                                           683 TACCGTCGACCTCGAGGGGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998; 23-JUN-1998; U13041. 24-JUN-1997; US-050667. (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                             175005 standard; DNA; 1122 BP 175005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X20513 standard: DNA; 651 BP. X20513;
                                                                                                                                                                                                                                                            06-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treponema pallidum WO9859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X20513
                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRI; 97.012121.02.

Recombinant DNA for expression of islet amyloid polypeptide - to develop prods. for use in diagnosis, study and treatment of develop prods. for use in diagnosis, study and treatment of develop prods. for use in diagnosis, study and treatment of disorders, e.g. diabetes and obbesity

Claim 6; Page 21-23; 46pp; English.

Claim 6; Page 21-23; 46pp; English.

Claim 6; Page 21-24; 46pp; English.

Claim 6; Page 21-25; 46pp; English.

Claim 6; Page 21-25; 46pp; English.

Claim 6; Page 21-26; 46pp; English.

Claim 6; Page 21-26; 46pp; English.

Claim 73795-804) of the ral mayloid and see also applied to the rale required by PCR amplification (see also applied by pCR amplification (see also applied plaque deposits in islet cells, fasting hyperglycaemia, applicating plaque deposits in islet cells, fasting hyperglycaemia, claim 6; place and diabetic glomerulosclerosis. They can be screened for treatments that modulate disease progression. Cell lines can be screened for treatments that inhibit human IAPP expression.

Claim 73795-809.
                                                                                           169 ATTAGAGCTCGCGGCCGCGAGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                               17 ACTAGATCTATTTATTGCACGCGGCCGCCATGGTGGATCCCCCGGGCTGCAGGAATTCGA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32 TGCACGCGCCCCCATGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGA 91
                                                                                                                                                                                                                                                                                143794/c

ID T47794 standard; DNA; 5356 BP.

AC T43794;

T43794;

T43794 standard; DNA; 5356 BP.

DT 18-FEB-1997 (first entry)

DE Plasmid pRIPHAT (rat insulin promoter-human IAPP transgene).

KW TYPE II dabetes mellitus; transgenic animal model; pancreas;

KW islet; beta cell; islet amyloid polypeptide; IAPP; hyperglycaemia;

KW 91ycouria; diabetic glomerulosclerosis; plasmid pRIPHAT; ds;
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note- "human IAPP coding sequence (Claim 7)" [861. .2580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.9%; Score 68; DB 1; Length 5356; 88.1%; Pred. No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene poly-A and RNA
                                                                                                                                        promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c/label= Albumin_intron/note= "human albumin intron 2575. 3119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/label= RIP-II_promoter
/note= "rat insulin II p
1589. .1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carty MD, Kreutter DK, Soeller WC; WPI; 97-021221/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "human GAPDH
termination region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- Poly-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/label= IAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 88.1
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-1996, IB0371.
24-APR-1996, IB0371.
23-MAX-1995, US-446935.
(PFIZ ) PFIZER INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric Homo sapiens
Chimeric Rattus sp.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9637612-A1
  80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminator
```

promoter

intron

NAME OF THE PROPERTY OF THE PR

ô

```
Homo sapiens.
WO9629338-A1.
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T39485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated uropathogenic E. coli nucleotide sequences - used to develop products for the detection of pathogenic E. coli and to develop products for the detection of pathogenic E. coli and to a licit an immune response to pathogenic E. coli E. coli and inmune response to pathogenic E. coli chi sequence represents a E. coli strain J96 contig containing this sequence represents a E. coli strain J96 contig containing of this sequence represents. The sequences, and represents a nucleic acid pathogenicity island (PAI) sequences of the invention are taken from pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI V. PAI IV is located at approximately 64 min (near pheV) con the E. coli chromosome and is approximately 94 min (at pheR) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit a protective immune response in an animal to the uropathogenic E. coli catrain J96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                      ö
                                                                                                                                                                                                                                                                                                     01-071-1998 (first entry)
E. coli J96 pathogenicity island contig #108.
E. toli J96 pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for detecting
                                                                                                                               47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                               0; Gaps
                                                                                                         Gaps
can also be used for det
in animals, and for the
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 752;
                                                                           Query Match
45.5%; Score 67.4; DB 1; Length 651;
Best Local Similarity 98.6%; Pred. No. 1.3e-14;
Matches 68; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 T;
                                         149 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
 infections, particularly syphilis. They can also be udiseases related to Borrelia infections in animals, a production of biosynthetic products such as enzymes. Sequence 651 BP; 180 A; 167 C; 152 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67.4; DE; Pred. No. 1.4e-0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 C;
                                                                                                                                                                                                                                                                                                                                                                                   28-MAY-1998.
21-NOV-1997; U21347.
14-CCT-1997; US-061953.
22-NOV-1996; US-031626.
(HUAA-) HUMAN GENOME SCI INC.
(UYMI-) UNIV WISCONSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi GH, Dillon PJ, Welch RA; WPI; 98-312461/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 A;
                                                                                                                                                                                                                                                                               V31294 standard; DNA; 752 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
048463/C
ID 048463 standard; DNA; 3792
AC 048463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  752 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GGGGGGGCC 115
                                                                                                                                                                                       107 GGGGGGCC 115
                                                                                                                                                                                                                 136 GGGGGGCC 144
                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGGGGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
                                                                                                                                                                                                                                                                                             V31294;
                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                      RESULT
V31294/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
G
                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                 셤
     88888
                                                                                                                                       ò
                                                                                                                                                               d
                                                                                                                                                                                          ò
```

```
New bacterial plasmid contg. heat sensitive replication system -
new bacterial plasmid contg. heat sensitive replication, used to
and marker gene opt. capable of chromosomal integration, used to
an activate specific gene or introduce heterologous gene
brample 2: Fig 9; 73pp; French
contained pGK12 (Appl.Environ.Microbiol., 48: 726 (1984)) contg. two
containing pGK12 (Appl.Environ.Microbiol., 48: 726 (1984)) contg. two
containing pGK12 (Appl.Environ.Microbiol., 48: 726 (1984)) contg. two
containing RepA - see Q48466 and Q48467), cut with Clar and Hparl and
the 3340bp fragment lacking the Car resistance gene was ligated to a
45bp Pvull fragment lacking the Car resistance gene was ligated to a
45bp Pvull fragment of pBluescript SK+ containing a multicloning
containing plasmid was designated pVE6004 (or pG+host4 - Q48463). It
contained at 28 deg.C.
contained at 28 deg.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 IGGIGGAICCCCCGGGCTGCAGGAATICGAIAICAAGCTIAICGAIACCGICGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 11. 196-443130/44.

No. 196-443130/44.

No. 196-443130/44.

No. 1solated human steroidogenesis acute regulatory protein gene - used isolated human steroidogenesis acute to detection of mutation(s) of this gene that cause congenital ripoid adrenal hyperplasia.

Claim 1; Pages 23-25; B9Pp; English.

The present sequence encodes the human steroidogenesis acute regulatory protein (hStAR). The hStAR gene can be analysed for regulatory protein (hStAR). The hStAR gene can be analysed for mutations to detect (e.g. prematally) genetic defects associated with congenital lipoid adrenal hyperplasia (CAH), or its transmission to children. CAH can be treated by protein or gene replacement therapy, which can also be used to prevent or treat hypercholesterolaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-MX-1997 (first entry)

Human steroidogenesis acute regulatory protein genomic DNA.

Human steroidogenesis; acute regulatory protein; hStAR; analysis;

mutation; detection; prenatal; genetic defect; congenital; protein;

lipoid adrenal hyperplasia; treatment; prevention; gene;

replacement therapy; hypercholesterolaemia; ds.
Plasmid pG+host4 containing Is replication system.

Temperature sensitive replication; antibiotic resistance marker gene site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%; Score 67.4; DB 1; Length 3792; 98.6%; Pred. No. 2.4e-14; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1249 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              742 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              552 C;
                                                                                                                                                                                                                                              16-SEP-1993.
12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG) INRA INST NAT RECH AGRONOMIQUE.
Gruss A, Maguin E;
WPI; 93-303478/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1249 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T39485 standard; DNA; 4226 BP. T39485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1996.
22-MAR-1996, U03896.
23-MAR-1995, GC-410540.
(REGC ) UNIV CALIFORNIA.
(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3483 GGGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maintained at 28 de Seguence 3792 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 GGGGGGCC 115
```

)

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47
                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                       ò
                                                                                                                                                                                                       d
                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                            쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gruss A, Maguin E;

MPI; 93-303478/38.

New bacterial plasmid contg. heat sensitive replication system -

New bacterial plasmid contg. heat sensitive replication system -

New bacterial plasmid contg. heat sensitive replication system -

The and marker gene, opt. capable of chromosomal integration, used to

Inactivate specific gene or introduce heterologous gene

Szemple 2; Frg 10, 73pp; French.

Plasmid pGK12 (Appl. Environ.Microbiol., 48; 726 (1984)) contg. two

Rample 2; Frg 10, 73pp; French.

Plasmid pGK12 (Appl. Environ.Microbiol., 48; 726 (1984)) contg. two

Antiblocit realstance marker genes was subjected to mutagenesis with

Ndroxylamine. A heat-stable mutant was isolated (coding for a heat-

sensitive RepA - see Q48466 and Q48467), cut with Clai and Hparl and

A45bp Pvull fragment lacking the Cm resistance gene was ligated to a

445bp Pvull fragment of pBluescript SK+ containing a multicloning

site, 77 and 73 promoters and sequencing primer blinding sites. The

resulting plasmid was designated pycB6004 (or pG-host4 - Q48463).

To facilitate cloning in E.coli, the 1.4kb Aval-AlwNI fragment of

pRRR322 (containing the origin of replication) was inserted into

Ramin-clasved pG+host4 to give pG+host5 (Q48464). The pBR322 ORI

allows maintenance of the plasmid in E.coli at 37 deg.C. while the

hat-sensitive ORI allows maintenance at 28 deg.C in gram-positive
                                                                                                                                                                                                                                                                                                                                                                                        4147 TAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 4206
                                                                                                                                                                                                                                                                                                                                                                  47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pG+host5 containing Ts replication system.
Temperature sensitive replication; antibiotic resistance marker gensite specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
A human adrenal cortex cDNA library was screened with a mouse StAR probe to isolate a 1.6 kb insert, including an ORF for a 285 residue protein. When it was cloned into pSPORT and expressed in COS-1 calls octransfected with pP450scc abd pADX, it increased the lavel of pregnenolone synthesis from cholesterol or 20-alpha-hydroxycholesterol.

Sequence 4226 BP; 940 A; 1132 C; 1144 G: 984 T·
                                                                                                                                                                                                                                                            Length 4226;
                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note- "origin of replication from pBR322"
2640. .4383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- b
//note= "from pGK12 (derived from pWV01)"
//note= "from pUB110"
//tag- c
//note= "from pUB110"
4787. 5234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                          Score 67.4; DB 1;
Pred. No. 2.5e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/standard_name= ORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 d
from pSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O48464/C

O48464/C

O48464, standard; DNA; 5234 BP.

O48464, standard; DNA; 5234 BP.

O48464, standard; DNA; 5234 BP.

DE Plasmid DG+host5 containing Ts re

KW Temperature sensitive replication

KW Site specific recombination; chrows synthetic.

ET Misc_feature 36. 1496

FT Misc_feature 36. 1496

FT Misc_feature 2640. 4383

FT Misc_feature 4384. 4786

FT MO9318164-A.

PR MO9318164-A.

A MO9318164-A.

A MO9318164-A.

A MO9318164-A.

PR MO9318164-A.

A MO9318164-A.

PR MO9318164-A.

A MO9318164-A.

PR MO9318164-A.

PR MO9318164-A.

A MO9318164-A.

A MO9318164-A.

PR MO9318164-A.

A MO93184 A MO9384

A MO9384
                                                                                                                                                                                                                                                          45.5%;
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4207 GGGGGGGCC 4215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 GGGGGGCC 115
                   88888888
                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            음
```

```
DESTRUCTION OF THE PROPERTY OF
                                                                                                                                                                                                         6473 TAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGTGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                             47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plasmid pG+host6 containing Ts replication system. Temperature sensitive replication; antibiotic resistance marker gen site-specific recombination; chromosomal integration; hactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Swedish-FAD APP targetting vector pMTI-2398.
Amyloid precursor protein; APP; human; gene targetting;
homologous recombination; transgenic mouse; transgenic animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 3e-14; DB 1; Length 6722; 0; Mismatches 1.
        Length 5234;
                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1503 G;
                                                                                        1;
Score 67.4; DB 1;
Pred. No. 2.7e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1278 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.5%; Score 67.4;
98.6%; Pred. No. 3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in gram-positive bacteria 6722 BP; 1971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X24730 standard; DNA; 12814 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q48465 standard: DNA; 6722 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.6
Matches 68; Conservative
                                                    Best Local Similarity 98.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6413 GGGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                                                                               4925 GGGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                      107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at 28 deg.C in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X24730;
21-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XXE DAG X
```

```
Example; page 104-113; 209pp; English.

This is the nucleotide sequence of London-FAD APP targetting
This is the nucleotide sequence of London-FAD APP targetting
the part-2453. The intendention provides a novel gene targetting
strategy that facilitates the introduction of one or more specific
mutations into any gene in a single double reciprocal homologous
crecombination step. The method has been used particularly for
introducing a humanised amyloid precursor protein (APP) gene into
codents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer's disease (AD).
Crodents for producing animal models of Alzheimer hybrid (m/APP) where
amino acid residues (66-77) of APP770 were encoded by human cDNA
crodents instead of mouse genomic exons 16-18). Within
these residues, only a maino acid differences exist between the
mouse and human proteins, i.e. dly-676 to Arg, Phe-681 to Thr and
croated using vector pMII-2433, the London mutation. i.e.
Created using vector pMII-2433, the London mutation. i.e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 99-181029/15.
P-PSDB; W97998, W97999.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.701.1999 (first entry)
Swedish/London-FAD APP targetting vector pWII-2454.
Swedish/London-FAD APP targetting vector pWII-2454.
Amyloid precursor protein; APP; human; gene targetting;
homologous recombination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pWII-2454;
London-FAD APP; Swedish-FAD APP; mutation; ss.
Formo sapiens.
Synthetic.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.5%; Score 67.4; DB 1; Length 15692; 98.6%; Pred. No. 4e-14; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2786 G;
                                                                                 /standard_name= "Swedish-FAD"
/note= "encodes W97999"
replace(4990,"")
                                                                                                                                                                           /standard_name= "London-FAD"
8223. .9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2730 C;
                                                                                                                                                                                                                                         /note= "encodes W97998"
                   Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2423 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X24732 standard; DNA; 15692 BP
X24732;
                                             . .5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Conservative
                                                                                                                                                                                                                                                                                                                               L8-AUG-1997; U14507;
L8-AUG-1997; WO-U14507.
                                                                  /*tag=
                                                                                                                                                             /*tag=
                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15692 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 12824 GGGGGGGC 12832
                                                                                                                                                                                                                                                                                           25-FEB-1999.
18-AUG-1997; U14507.
                                                                                                                                                                                                                                                                                                                                                              (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                        W09909150-A1
                                        mat_peptide
                                                                                                                                                                                                     mat_peptide
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                     mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
X24732
X24732
AC X24732
DT 21-JUN
DE SWEGLS
KW Amyloi
KW Annimol
KW London
KW London
COS Homo S
OS Synthe
                                                                                                                                                                                                                                                                                                                                                                                        Wirak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                          é
  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graease the nucleotide sequence of Swedish-FAD APP targetting This is the nucleotide sequence of Swedish-FAD APP targetting This is the nucleotide sequence of Swedish-FAD APP targetting convector part-2398. The introduction of one or more specific strategy that facilitates the introduction of one or more specific compliantion step. The method has been used particularly for introducting a humanised amyloid precursor protein (APP) gene into introducing a humanised amyloid practicularly for codents for producing animal models of Alzheimer's disease (AD).

Crodents for producing animal models of Alzheimer's disease (AD).

Crodents for producing animal models of Alzheimer's disease (AD).

ESS401 and ESS403) have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse APP gene was modified to encode a mouse/human hybrid (m/AAPP) where amino acid residues 666-770 of APP770 were encoded by human cDNA.

Created containing a humanised beta-amyloid domain. In line ESS007, created using vector pWrI-238, the Exwedish mutation. i.e. containing a humanised amyloused. The targetted Swedish in the containing a humanised and introduced. The targetted Swedish in the containing a humanised and introduced. The targetted Swedish in the containing a humanised and introduced. The targetted Swedish intervention and containing a humanised and containin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9886 TAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 9945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 99-181029/15.
P-PSDB; W97997, W97998.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised anyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      m/happ gene expressed m/happ protein at levels approaching those observed for mouse APP in brain.

Sequence 12814 BP; 1865 A; 1850 C; 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUN-1999 (first entry)
London-FAD APP targetting vector pMTI-2453.
Amyloid precursor protein; APP; human; gene targetting;
homologous recombination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pMTI-2453;
London-FAD APP; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.5%; Score 67.4; DB 1; Length 12814; 98.6%; Pred. No. 3.7e-14; ive 0; Mismatches 1; Indels 0;
animal model; Alzheimer's disease; vector; pMTI-2398;
Swedish-FAD APP; mutation; ss.
Homo sapiens.
Synthetic
                                                                                                                                                           /standard_name= Swedish-FAD APP
/note= "encodes W97997"
5369. .6160
                                                                                                                                                                                                                                    /*tag= b
/note= "encodes W97998"
                                                                                     Location/Qualifiers
1932, .2276
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X24731 standard; DNA; 15692 BP. X24731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 98.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                        18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
(FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9946 GGGGGGCC 9954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
                                                                                                                                                                                                                                                                               W09909150-A1
                                                                                                                    mat_peptide
                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                       3-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Wirak DO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ношо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X24731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEW KEN
         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
```

0; Gaps

ŀ

2541 T;

.)

4807.

```
Example; Page 114-123; 209pp; English.

Example; Page 114-123; 209pp; English.

This is the nucleotide sequence of Swedish/London-FAD APP targetting vector puri-254. The invention provides a novel gene targetting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous crecombination step. The method has been used particularly for introducing a humanised anyloid precursor potein (APP) gene into codents for producing animal models of Alzheimer's disease (AD).

Introducing a humanised anyloid precursor protein (APP) gene into codents for producing animal models of Alzheimer's disease (AD).

Ending a papel of transgenic mice (inter ESS103), ESS103, ESS10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-FSDB; W97998, W98000.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2542 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2783 G;
                                                                                                                          /standard_name- "Swedish-FAD"
replace(4989,"")
/standard_name- "London-FAD"
8223. 9023
/*tag- b
/note- "encodes W97998"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2731 C;
                        /*tag= a
/note= "encodes W98000"
replace(4849,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2423 A;
                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                  25-FEB-1999.
18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
(FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15692 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 99-181029/15
                                                                                                                                                                                                                                                                                    WO9909150-A1
mat_peptide
                                                                                                                                                                                                           mat_peptide
                                                                                                                                                          mutation
                                                                              mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease
                                                                                                                                                                                                                                                                                                                                                                                                                         Wirak
```

ö 0; Gaps 45.5%; Score 67.4; DB 1; Length 15692; 98.6%; Pred. No. 4e-14; Live 0; Mismatches 1; Indels 0; Best Local Similarity 98.6 Matches 68; Conservative Query Match

Db 12764 TAGTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACGGTGCACCTCGA 12823 47 IGGIGGAICCCCCCGGGCTGCAGGAAITCGAIAICAAGCIIAICGAIACCGICGACCICGA 106 ò

107 GGGGGGGCC 115

à

Db 12824 GGGGGGGCC 12832

Search completed: May 29, 2000, 21:58:27 Job time: 38175 sec

ĝ.			1,	
r:			<b>₩</b> 1	
*			Say II Say III Say III	
			n de Terr	
iet.			•	· .
We.			*	
100				
#/ 				
£				
• .				
₩. ·			Na Strain Na	
Si 				
đ.				<u>ئۆ</u>
			.71	
	현실 사용하는 사람들이 되었다. 그는 사용하는 사용하는 사용하는 사용하는 사용하는 사용하는 것이다. 1980년 - 1980년 1일 대한민국 (1987년 1일 대한민국 (1987년 1987년			
£				
70.0				
\$** 1			and the second	
			i.	
1				3
				, d
1				
16. 18.				
<b>3</b> 6			*	<b>3</b>
مقر			e	
	kan di kalangan di Kabupatèn Bandaran Kabupatèn Bandaran Kabupatèn Bandaran Kabupatèn Bandaran Kabupatèn Banda Manggalan Kabupatèn Bandaran Kabupatèn Bandaran Kabupatèn Bandaran Kabupatèn Bandaran Kabupatèn Bandaran Kabup			. 3
7				•
ì				
**				
•				
				•
*				
C)				
Š				
				स.
				- <del>2</del>
				· V
¥.				
				i di
h M		en e		35 19.
*				
		gir <b>v</b> aran kan dari		4
				i A
*				
a v				
				, uta-

Н

```
May 29, 2000, 22:09:00 ; Search time 621.83 Seconds (without alignments) 30.937 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, Appli
1, Appli
2, Appli
2, Appli
3, Appli
3, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10,
Sequence 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                           148
1 GGCCAAAAATTGAAAAACTA......TTGTTTTTTGTGGGCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sednence Sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence Sequence Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-967-101-121
US-08-952-341-121
US-08-302-752-1
US-08-302-752-1
US-08-302-752-3
US-08-992-334-2
US-08-992-334-3
US-08-992-334-3
US-08-992-334-3
US-08-992-334-3
US-08-302-752-3
US-08-302-752-3
US-08-302-752-3
US-08-302-752-3
US-08-46-1
US-08-46-1
US-08-46-1
US-08-46-1
US-08-46-1
US-08-46-1
US-08-198-46-1
US-08-198-46-1
US-08-198-10-1
US-08-198-10-1
US-08-10-11-113
US-08-96-31-1
                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                    230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    nucleic search, using sw model
                                                                                                                                                                                                                                                IDENTITY_NUC Gapox 1.0
                                                                                                                                                                             US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1023
1023
2150
2150
2150
834
834
6505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3792
3792
3792
4016
5234
6722
6722
685
685
685
4164
41164
41164
41164
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                 Scoring table:
                                                                    OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                Seguence:
                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0 0 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      000000
```

Sequence

```
ö
                                                                                                                                                                                           Appli
Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appl
Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
         Sequence 1
Sequence 3
Sequence 3
Sequence 3
Sequence 6
Sequence 6
Sequence 6
Sequence 6
Sequence 6
                                                                                                                                                                                                                                                                                                                                                                                   Sequence Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3
Sequence 1
Sequence 4
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 121, Application US/08967101
Fatent No. 5840340
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TILLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA HURMITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION BAILARS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION NUMBER: US/08/967,101
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING APPLICATION DATA:
ATORNEY/AGENT INFORMATION:
NAME: PICCHE, Edmund R.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENDTH: 793 base pairs
TTPE: NUCLEIC caid
STRANDENESS: sinqle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.2%; Score 68.4; DB 3;
llarity 87.2%; Pred. No. 3.8e-14;
Conservative 0; Mismatches 11;
US-08-967-101-116
US-08-52-541-116
US-08-464-051-3
US-08-464-051-3
US-08-462-488-3
US-08-260-452-8
US-08-260-452-8
US-08-361-1970-8
US-08-387-719-8
US-08-325-071-62
US-08-325-071-62
US-08-343-733A-1
US-08-343-733A-1
US-08-465-388-35
US-08-465-388-35
US-08-667-8098-3
US-08-667-8098-3
US-08-667-8098-3
US-08-667-8098-3
US-08-667-8098-3
US-08-667-8098-3
US-08-667-8098-3
   -08-967-101-116
-08-592-541-116
-08-011-398B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-967-101-121
   CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 75; Conserv
   \begin{array}{c} \mathbf{u} \\ \mathbf{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-08-967-101-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02110
   4444
      00000000000
```

```
47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.5%; Score 67.4; DB 4; Length 3792; 98.6%; Pred. No. 1.3e-13; i.ve 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                            CAPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTION NUMBER: VS/08/992,334
FILING DATE: 12-DEC-1994
PRIOR APPLICATION NUMBER: C1994
PRIOR APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION NUMBER: FR FR92/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PROUGH INFORMATION:
NAME: PROUGH INFORMATION:
TELEFANG (626) 779-9900
TELEFAN: (626) 779-9900
TELEFAN: (626) 779-9900
TELEFAN: (626) 779-9900
TELEFAN: C626) 779-9800
TREADERATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
                                    ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 1, Application US/08302752; Patent No. 6025190; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/Ms-1.SOFTWARE: Patent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 98.6
Matches 68; Conservative
                                                                            CITY: Pasadena
STATE: California
COUNTRY: United States
2IP: 91105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TH
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3483 GGGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; IMMEDIATE SOURCE:
; CLONE: pG+host4
US-08-992-334-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: circu
MOLECULE TYPE: DN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-08-302-752-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 GGIGGAICCCCCGGGCCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 107
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 GGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACGTTGTGGATGCTCGAGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

46.2%; Score 68.4; DB 4; Length 793;
Best Local Similarity 87.2%; Pred. No. 3.8e-14;
Matches 75; Conservative 0; Mismatches 11; Indels
                                                                                                                                                                                                                  Sequence 121, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02110
COMPUTER READABLE FORM:
MEDION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108 GGGGGCCTAACTAACTATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 GGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                       108 GGGGGCCTAACTAACTATTTTGTT 133
                                                                                                                             59 GGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic) US-08-592-541-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                             RESULT 2
US-08-592-541-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                         ö
                                                                                                                             g
              ò
```

```
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Miler, Walter L.

APPLICANT: Lin, Dong
APPLICANT: Struct
APPLICANT: ASSOCIATED WITH CONGENITAL LIPOID ADREND.
AUTHOR ASSOCIATED WITH CONGENITAL LIPOID ADREND.
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STRET: 5 Palo Alto
STATE: CA
CITY: Palo Alto
CITY: 10.56.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.05.01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 IGGIGGAICCCCCGGGCTGCAGGAAITCGAIATCAAGCITAICGAIACCGICGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 45.5%; Score 67.4; DB 5; Best Local Similarity 98.6%; Pred. No. 1.3e-13; Matches 68; Conservative 0; Mismatches 1;
                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION UNBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION NUMBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTER STICS:
LENGTH: 3792 base pairs
LENGTH: 3792 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
WOLECULE TYPE: DNA (genomic)
US-08-302-752-1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-410-540-3
; Sequence 3, Application US/08410540
; Patent No. 5807678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                              FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3483 GGGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

```
3937 TAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 3996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-992-334-2/C

Sequence 2, Application US/08992334

Patent No. 5919678

SEQUENCE IN OFFICANTION:

APPLICANT: Maguil, Emmanuelle

TITLE OF INVENTION:

TITLE OF INVENTION:

CORRESPONDENCE 3

CORRESPONDENCE ADDRESS:

ADDRESSE: Christle Parker & Hale, LLP

STREET: 350 West Colorado Boulevard, Suite 500

CITY: Pasadema

STATE: California

COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 2956..2957
COTHER INFORMATION: /note- "interruption of sequence data"
US-08-410-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: -
LOCATION: 1433..1434
OTHER INFORMATION: /note= "interruption of sequence data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: /note= "interruption of sequence data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.5%; Score 67.4; DB 2; Best Local Similarity 98.6%; Pred. No. 1.3e-13; Matches 68; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2956..2957
                                                           exon
1098..1283
                                                                                                              .exon
1620..1733
                                                                                                                                                                    exon
2047..2174
                                                                                                                                                                                                                          exon
2267..2425
                                                                                                                                                                                                                                                                               exon
2567..2751
                                                                                                                                                                                                                                                                                                                                     exon
2828..2921
                                                                                                                                                                                                                                                                                                                                                                                          exon
3031..3765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3997 GGGGGGGCC 4005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GGGGGGGCC 115
HYPOTHETICAL:
ANTI-SENSE: NC
FEATURE:
NAME/KEY: ex
LOCATION: 10
```

; 0

```
47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-08-992-334-3/c
| Sequence 3, Application US/08992334
| Patent No. 591964|
| Patent No. 591964|
| GENERAL INFORMATION:
| APPLICANT: Magulin, Emmanuelle
| TILLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
| TITLE OF INVENTION: PLASMID |
| NUMBER OF SEQUENCES: 3 CORRESPONDENCE ADDRESS: ADDRESSE: Christie Parker & Hale, LLP |
| STREET: 350 West Colorado Boulevard, Suite 500
                                                                                                                                                                                           Score 67.4; DB 5; Length 5234; Pred. No. 1.4e-13; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Pasadena STATE: California COUNTR: United States ZIP: 91105
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/992,334 FILING DATE: 17-DEC-1997
CLASSIFICATION: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRICH APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRICH PAPLICATION NUMBER: F FF92/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Frout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-08-992-334-3
                                                                                           MOLECULE TYPE: DNA (genomic) US-08-302-752-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (626) 795-9900
TELEFAX: (626) 577-8800
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                  Query Match
Best Local Similarity 98.6%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 6722 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                     5234 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pain
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                    4925 GGGGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                       107 GGGGGGCC 115
                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 67.4; DB 4; Length 5234; Pred. No. 1.4e-13; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOSEPH CALL OF APPLICATION US/08302752

Sequence 2, Application US/08302752

Sequence 2, Application US/08302752

Sequence 2, Application US/08302752

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF TYPE: FLOPPY disk
COMPUTER READABLE FORM:
COMPUTER: IMP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentION Nelsone #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/08/302,752
                                                                                                            OPERATING SISTEM:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION NUMBER: US/08/992,752
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 24-DEC-1994
PRIOR APPLICATION NUMBER: PEC-1994
PRIOR APPLICATION NUMBER: PEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PEC-1994
FILING DATE: 12-MAR-1993
PRIOR APPLICATION NUMBER: C9958
REGISTRATION NUMBER: C9958
REGISTRATION NUMBER: 20958
REGISTRATION NUMBER: 20958
REGISTRATION NUMBER: C9958
REGISTRATION NUMBER: C99500
INPORMATION (626) 795-9900
INFORMATION ECONOMINICATION INFORMATION:
TELEPHONE: (626) 795-9900
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARACTERISTICS:
LENDTH: 5234 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUBBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUBBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 2:
                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) US-08-992-334-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.6%;
Matches 68; Conservative
            ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4925 GGGGGGGC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
```

8 ò

```
5654 GGGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 5713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.2%; Score 65.4; DB 3; Length 9318; 98.5%; Pred. No. 7.6e-13;
                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPANING SYSTEM: PC-DOS/MS-DOS
SOFTWAREN PAPILCATION 'DATA:
APPLICATION 'DATA:
APPLICATION NUMBER: US/08/793,610
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
PRIOR APPLICATION NUMBER: DE P 44 31 973.8
PRIOR APPLICATION NUMBER: DE P 50 3952.1
FILING DATE: 07 FEB-1995
PRIOR APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07 FEB-1995
PRIOR APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07 FEB-1995
PRIOR APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 10 ANG-1995
ATTONNEY/AGEPT INFORMATION:
NAME: ADDITION NUMBER: DE 195 03 952.1
ATTONNEY/AGEPT INFORMATION:
NAME: ADDITION NUMBER: DE 195 03 952.1
ATTONNEY/AGEPT INFORMATION:
NAME: ADDITION NUMBER: DE 195 03 952.1
ATTONNEY/AGEPT INFORMATION:
NAME: ADDITION NUMBER: DE 195 03 175
655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 56, Application US/08463115
Patent No. 5703221
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
ALLIAM JOHN MARTIN
TITLE OF INVENTION:
TORRESPONDENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERENCE/DOCKET NUMBER: 91,105
REFERENCE/DOCKET NUMBER: P1614-7007
TELECHONE: (202)638-5000
INFORMATION: (202)638-4810
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite:4700
CITY: Los Angeles
STATE: Callfornia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 98.5
Matches 66; Conservative
                                                              COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 90071-2066
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         circular
                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circul MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5714 GGGGGCC 5720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-463-115-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: BAUM, CHRIStopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEROF
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 6722;
                  Length 6722;
                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
                    Query Match 45.5%; Score 67.4; DB 4;
Best Local Similarity 98.6%; Pred. No. 1.5e-13;
Matches 68; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.5%; Score 67.4; DB 5; Best Local Similarity 98.6%; Pred. No. 1.5e-13; Matches 68; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THERMOSENSIBLE PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FK/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-302-752-3/C
US-08-302-752-3/C
Sequence 3, Application US/08302752
PATENT NO. 6025190
JAPLICANT:
TITLE OF INVENTION: THERMOSENSIBI
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
'~~wonTHER: IBM PC compatible
'~~wonTHER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/08793610 Patent No. 5858744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                         6413 GGGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6413 GGGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 GGGGGGGCC 115
                                                                                                                                                                                                                          107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
US-08-793-610-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-302-752-3
```

g õ

ò

```
47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCITAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08204675

Sequence 1, Application US/08204675

Patent No. 5677170

GENERAL INFORMATION:
APPLICANT: Boeke, Jef D.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES:
ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
COUNTRY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
42.4%; Score 62.8; DB 2; Length 68
Best Local Similarity 92.8%; Pred. No. 2.7e-12;
Matches 64; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                       FILING DATE: June J.
CLASSIPICATION 1435
PRIOR APPLICATION DATA: Including application PRIOR APPLICATION DATA: Including application PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: 08/15/811
FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/76/81,502
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/76,914
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/76,039
FILING DATE: September 20, 1991
APPLICATION NUMBER: 32,327
REJERATION PROMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 213/300
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,675
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: US-08-465-388-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208 GGGGGGGNC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
US-08-204-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 IGGIGGAICCCCCGGGCIGCAGGAAITCGAIAICAAGCITAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
42.4%; Score 62.8; DB 2; Length 68:
Best Local Similarity 92.8%; Pred. No. 2.7e-12;
Matches 64; Conservative 0; Mismatches 5; Indels
                                                                                                FILING DATE: out.

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 07/15,811
APPLICATION NUMBER: 07/16,814
FILING DATE: MAY 22, 1991
APPLICATION NUMBER: 07/76,039
FILING DATE: MAY 23, 1991
APPLICATION NUMBER: 07/76,039
FILING DATE: SEPTEMBER: 07/76,1091
APPLICATION NUMBER: 20, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Walburg, Richard J.
REGISTRATION NUMBER: 213/301
TELECOMONICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELERA: 67-3510
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 685 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-08-465-388-56
Sequence 56, Application US/08465388
Sequence 56, Application US/08465388
SEQUENCE 56, Application US/08465388
SERENTAL INFORMATION
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
OPERATING SYSTEM: IBM P.C. DOS 5.0 SOTTWARE: FastSeq Version 1.5 CURRENT APPLICATION DATA: US/08/463,115 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: US-08-463-115-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 GGGGGGNC 216
```

δ

ö

Gaps

Ş

```
2005 TCGAACAIGTTCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGG 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 TIGAAAAACTAGAICTAITIAIIGCACGCGGCCGCCAIGGIGGAICCCCCGGGCIGCAGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jel Delita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,364
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2065 AATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
40.3%; Score 59.6; DB 3;
Best Local Similarity 75.5%; Pred. No. 5.2e-11;
Matches 74; Conservative 0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 AATICGAIAICAAGCIIAICGAIACCGICGACCICGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PAPLLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENY INFORMATION:
NAME: RAGISTRATION NUMBER: 32,141
REFIRENCE/DOCKET NUMBER: 01107.45501
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELETAX: 107430 BBMB UT
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08796364
Patent No. 5968785
                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                             SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
           INFORMATION FOR SEQ ID NO:
                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ctrcular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D.C.
                                                                                                                                                                                                                                                                                              ; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: PAT-1
US-08-660-754-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-796-364-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2005 TCGAACATGTTCACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGG 2064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 TIGAAAAACTAGAICTATITATIGCAGGGGGGGCGCCAIGGIGGAICCCCGGGGTGCAGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 40.3%; Score 59.6; DB 1; Length 4164; Best Local Similarity 75.5%; Pred. No. 5.2e-11; Matches 74; Conservative 0; Mismatches 24; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08660754

| Sequence 1, Application US/08660754
| Patent No. 5843712
| Patent No. 5843712
| GENERAL INFORMATION:
| APPLICANT: Boeke, Jef D. |
| APPLICANT: Braiterman, Lelita T. |
| TITLE OF INVENTION: In Vitro Transposition of Artificial TITLE OF INVENTION: I Transposons |
| TITLE OF INVENTION: I NOTICE: 7 |
| TORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Banner, Birch, McKie, and Beckett STREET: 1001 G Street, N.W. |
| CITY: Washington COUNTRY: U.S.A. |
| STREET D.C. |
| STATE: D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin BPC-DOS/MS-DOS
SOFTWANE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,754
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE:
CLASSIFICATION: 335
PRIOR APPLICATION NUMBER: US 08/204,675
FILING DATE:
NAME: Kagan, Sarah A.
REGISTATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION UNBER: 01107.45501
TELECAX: 202.508.9299
TELEEX: 197430 BBMB UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2065 AATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 AATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUBBER: 32,141

REFERENCE/DOCKET NUMBER: 01107.45501

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202.508.910

TELEFAX: 202.508.910

TELEX: 194430 BBMB UT

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4164 base pairs

TYPE: nucleic acid

STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
MATI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
US-08-204-675-1
```

ò

ò

```
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: PAT-1
US-08-796-364-1
```

ó 0; Gaps Query Match

40.3%; Score 59.6; DB 4; Length 4164;
Best Local Similarity 75.5%; Pred. No. 5.2e-11;
Matches 74; Conservative 0; Mismatches 24; Indels 0.

δŏ a ŏ

Search completed: May 29, 2000, 22:09:05 Job time: 38746 sec

```
148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                    May 30, 2000, 09:48:30 ; Search time 2276.24 Seconds (without alignments) 290.102 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                     148
1 GGCCAAAATTGAAAACTA......TTGTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10285240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pending_Patents_NA:*

1: /cgnl_6/ptodata/1/pna/PCTUS_COMB.seq:*
2: /cgnl_6/ptodata/1/pna/US06_COMB.seq:*
3: /cgnl_6/ptodata/1/pna/US07_COMB.seq:*
4: /cgnl_6/ptodata/1/pna/US08_COMB.seq:*
5: /cgnl_6/ptodata/1/pna/US081A_COMB.seq:*
6: /cgnl_6/ptodata/1/pna/US081A_COMB.seq:*
7: /cgnl_6/ptodata/1/pna/US081A_COMB.seq:*
8: /cgnl_6/ptodata/1/pna/US081A_COMB.seq:*
9: /cgnl_6/ptodata/1/pna/US082A_COMB.seq:*
10: /cgnl_6/ptodata/1/pna/US082A_COMB.seq:*
11: /cgnl_6/ptodata/1/pna/US082A_COMB.seq:*
12: /cgnl_6/ptodata/1/pna/US082A_COMB.seq:*
13: /cgnl_6/ptodata/1/pna/US084A_COMB.seq:*
14: /cgnl_6/ptodata/1/pna/US084A_COMB.seq:*
15: /cgnl_6/ptodata/1/pna/US084A_COMB.seq:*
16: /cgnl_6/ptodata/1/pna/US084A_COMB.seq:*
17: /cgnl_6/ptodata/1/pna/US084A_COMB.seq:*
18: /cgnl_6/ptodata/1/pna/US085_COMB.seq:*
19: /cgnl_6/ptodata/1/pna/US085_COMB.seq:*
10: /cgnl_6/ptodata/1/pna/US085_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgnl_6/ptodata/1/pna/US087C_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088B.COMB.seq:*
/cgnl_6/ptodata/1/pna/US088B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088C_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgnl_6/ptodata/1/pna/US089C_COMB.seq:*/cgnl_6/ptodata/1/pna/US089D_COMB.seq:*/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*/cgnl_6/ptodata/1/pna/US089F_COMB.seq:*/cgnl_6/ptodata/1/pna/US089F_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'ptodata/1/pna/US087C_COMB.seq:*
'ptodata/1/pna/US088A_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ptodata/1/pna/US088D_COMB.seq:*
ptodata/1/pna/US089A_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ptodata/1/pna/US089G_COMB.seq:*/
/ptodata/1/pna/US089H_COMB.seq:*/
/ptodata/1/pna/US0891_COMB.seq:*/
/ptodata/1/pna/US090A_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptodata/1/pna/US090B_COMB.seq:*
ptodata/1/pna/US090C_COMB.seq:*
ptodata/1/pna/US090D_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /ptodata/1/pna/US089B_COMB.seg:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn1_6/ptodata/1/pna/US092A_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5142629 seqs, 2230885800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                 US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn1_6/
/cgn1_6/
/cgn1_6/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn1_6/j
/cgn1_6/j
/cgn1_6/j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn1_6,
                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                         OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                    Run on:
```

```
/cgnl_6/ptodata/1/pna/US6004A_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6004A_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6004C_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6005_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6005_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
/cgnl_6/ptodata/1/pna/US6008B_COMB.seq:*
                                                                                                                                                            /cgnl_6/ptodata/1/pna/USO93F_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO94A_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO94C_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO95_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO00_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO00_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO01A_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO01A_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO01A_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO01A_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO01A_COMB.seq:*
/cgnl_6/ptodata/1/pna/USO01A_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgnl_6/ptodatts/1/pns/US6010A_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6010A_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6010B_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6011B_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6012A_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6012A_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6013A_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6013B_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014B_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014B_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014B_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014C_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014C_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014C_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014C_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6014C_COMB.seq:
/cgnl_6/ptodatts/1/pns/US6016A_COMB.seq:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgnl_6/ptodata/1/pna/US07_NEW_COMB.seq
/cgnl_6/ptodata/1/pna/US08_NEW_COMB.seq
/cgnl_6/ptodata/1/pna/US09_NEW_COMB.seq
/cgnl_6/ptodata/1/pna/US60_NEW_COMB.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn1_6/ptodata/1/pna/US06_NEW_COMB.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgnl_6/ptodata/1/pna/US6002C_COMB.seq:
/cgnl_6/ptodata/1/pna/US6003A_COMB.seq:
/cgnl_6/ptodata/1/pna/US6003B_COMB.seq:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgnl_6/ptodata/1/pna/US6016C_COMB.seq.
cgnl_6/ptodata/1/pna/US6017A_COMB.seq.
/cgnl_6/ptodata/1/pna/US6017B_COMB.seq.
/cgnl_6/ptodata/1/pna/US6017C_COMB.seq.
/cgnl_6/ptodata/1/pna/US6018A_COMB.seq.
/cgnl_6/ptodata/1/pna/US6018B_COMB.seq.
/cgnl_6/ptodata/1/pna/US6018C_COMB.seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19_COMB.seq:
/ognl_6/ptodata/1/pna/US093B_COMB.seq
/cgnl_6/ptodata/1/pna/US093C_COMB.seq
/cgnl_6/ptodata/1/pna/US093D_COMB.seq
                                                                                                                          'ptodata/1/pna/US093E_COMB.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102:
104:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 7, Sequence 8,
SUMMARIES	QI	US US
	DB	28
	Query Match Length DB	148 149
	Query Match Le	8 100.0 17. 92.6
, do	N Ma	120
	ø	8.7

0000000000

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GGCIGCAGGAATICGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGGGCGGCCGCTGGTGGATCCCCCG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-935-377-8
US-08-935-377-8

J. Sequence 8, Application US/08935377

Sequence 8, Application US/08935377

Sequence 8, Application US/08935377

APPLICANT: Zauderer, Maurice

TILE OF INVENTION: T Cells Specific for Target Antigens and

TILLE OF INVENTION: Vaccines Based Thereon

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C

STREET: 1100 New York Avenue, N.W., Suite 600

CITY: Washington

CITY: Washington

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                               Length 148;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USER
ZIP: 20005
COMPUTER: EDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EDAP DISK
COMPUTER: EDAP FOLDS
CORPUTER: DEAP COMPUTER
CONTROL SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RElease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: STEFFE ELECKEN STEFFE RELECTORMUNCATION NUMBER: 1821.0010000/EKS/CMB
REGISTRATION NUMBER: 36,688
REGISTRATION NUMBER: 36,088
REJERENCE/POCKET UNBER: 1821.0010000/EKS/CMB
TELECOMMUNCATION INFORMATION:
TELECOMMUNCATION INFORMATION:
TELECOMMUNCATION FOR SED ID NO: 8:
SEQUENCE CHRRACTERÍSTICS:
SAUGNOE CHRRACTERÍSTICS:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
RELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 148 base pairs
TELEN INCHEL acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 148; DB 28;
Best Local Similarity 100.0%; Pred. No. 1e-39;
Matches 148; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 AACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 149 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linea
                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-935-377-8
                                                                                                                                                                                                                                                            , MOLECULE TYPE:
US-08-935-377-7
                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                           Sequence 11, Appli
Sequence 51, Appl
Sequence 595, App
Sequence 8570, Ap
Sequence 8570, Ap
Sequence 8523, Ap
Sequence 8523, Ap
Sequence 8523, Ap
Sequence 8595, Ap
Sequence 9309, Ap
Sequence 2334, Ap
Sequence 2495, Ap
Sequence 2255, Ap
Sequence 2255, Ap
Sequence 2255, Ap
                                                                                                                                                                                                                                     Sequence 121, .....
Sequence 121, App
Sequence 121, App
                                                                                                                                                               Sequence 121
                                                                                                                                                                                    Sequence 1
Sequence 1
Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence (
                                                                                                Sequence Sequence A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITT: Meahington
STATE: D.C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPATIBLE COPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/935,377 FILING DATE: 22-SEP-1997 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
         US-08-935-377-6
US-08-935-377-6
US-09-221-107-91
US-09-221-107-91
US-09-221-107-91
US-09-221-107-91
US-08-693-359-121
US-08-69-359-121
US-08-69-359-121
US-08-509-359-121
US-08-509-359-121
US-08-509-359-121
US-08-124-698-121
US-08-124-698-121
US-08-124-698-121
US-08-124-698-121
US-08-124-698-121
US-08-124-698-121
US-09-124-698-121
US-09-124-698-121
US-09-124-698-121
US-09-321-694-8523
US-09-312-782-8550
US-09-312-782-8550
US-09-312-782-8553
US-09-312-782-8553
US-09-312-782-8553
US-09-312-782-8553
US-09-312-694-8553
US-09-312-782-8553
US-09-312-782-8553
US-09-312-782-8553
US-09-312-782-8553
US-09-312-694-8553
US-09-312-694-8553
US-09-312-694-8553
US-09-312-782-3344
US-09-312-694-3334
US-09-312-334-3360
US-09-328-351-2255
US-09-328-351-2255
US-09-328-351-2255
US-09-328-351-2255
US-09-328-351-2255
US-09-328-351-2255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-08-935-377-7
```

à g ò g ò g

```
Sequence 91. Application US/09123912A
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Wing Tongtong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 210121.455C1
CURRENT APPLICATION NUMBER: US/09/123,912A
CURRENT FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                           Sequence 6, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1103 New York Avenue, N.W., Suite 600
CITTY Washington
STATE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 132; DB 28; Length 145;
Pred. No. 2.4e-34;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      121 CTAACTAATTTTGTTTTTGGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 AACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AACTAATTTTGTTTTTGTGGGCCCGGCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.2%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.0°
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-123-912-91
                                                   RESULT 4
US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
ద
                                                   ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ĥ
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATG--GTGGATCCCC 58
                                                                                      1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATG-GTGGATCCCCC 59
                                                                                                                                                                                                                                                                                                                                                                                                          for Target Antigens and
                Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 150;
              Query Match 92.6%; Score 137; DB 28; Length 14
Best Local Similarity 99.3%; Pred. No. 5e-36;
Matches 148; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: D. C. COUNTRY: U.S. COUNTRY: U.S. COUNTRY: D. C. COUNTRY: MADIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION UNBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2560
TELEFXX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.9%; Score 136; DB 28; 98.7%; Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                             Sequence 9, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zaudecror, Maurice
TITLE OF INVENTION: T Cells Specific for Te
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                             120 TAACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                121 TAACTAATTTTGTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 98.7
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: lir; MOLECULE TYPE: US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                    US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                  Query Match
                                                                                                                                                                                                                                                                                                                     RESULT
```

g ö g ö

ô

ä

Gaps

```
331 tcaacgaattccaccacactggactagtggatccccggggctgcaggaattcgatatcaa 390
                                                                                                                                                       Sequence 91, Application US/09221107
Sequence 91, Application US/09221107
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TONGTONG
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER
FILE REFERENCE: 21011.455C2
CURRENT APPLICATION NUMBER: US/09/221,107
CURRENT FILING DATE: 1998-12-22
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 91
LENGTH: 858
                                     83 GCTTATCGATACCGTCGACCTCGAGGGGGGGCC 115
                                                             or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Where n is a, c, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ϋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
LOCATION: (664)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (667)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (683)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :ON: (711)
INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION: (760)
INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (591)
OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base LOCATION: (765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified_base LOCATION: (570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
                                           ŏ
                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified_base
LOCATION: (820)
CCTATION: UNFORMATION: Where n is a, c, g or t
US-09-123-912-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            占
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (804)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Where n is a, c, NAME/KEY: modified_base
LOCATION: (792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (809)
OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (817)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                     OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
LOCATION: (683)
UNTER INFORMATION: Where n is a,
NAME/KEY: modified_base
LOCATION: (711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (759)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Where n is a, NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                              ą
                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                             LOCATION: (591)
OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Where n is NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                    LOCATION: (655)
OTHER INFORMATION: Where n is
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Where n is NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                      ION: (667)
INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Where n is NAME/KEY: modified_base
                 NUMBER OF SEQ ID NOS: 114 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
LOCATION: (801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified_base
LOCATION: (760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
                                                                                                                                 FEATURE:
NAME/KEY: modified_base
                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
```

Query Match
Best Local Similarity 84.9%; Pred. No. 1.6e-13;
Matches 79; Conservative 0; Mismatches 14; Indels 0

LOCATION: (787) OTHER INFORMATION: Where n is

NAME/KEY: modified_base

NAME/KEY: modified_base LOCATION: (792)

```
47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 TAGTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 145
                                                                                                                    RESULT 8
US-08-377-383-4
; Sequence 4, Application US/08377383
; GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
Method of Determining Base Sequence of
TITLE OF INVENTION:
TITLE OF TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08693573
GENERAL INFORMATION:
APPLICANT: FURAMI, Padashi,
APPLICANT: FURAMI, Padashi,
APPLICANT: KOJIMA, Makiko
TITLE OF INVENTION: Method of Determining Base Sequence of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARRY CUSHMAN
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Cushman Darby & Cushman STREET: Ninth Floor, 1100 New York Avenue, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 46.9%; Score 69.4; DB 13; Best Local Similarity 87.4%; Pred. No. 2.9e-13; Matches 76; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READELE FORM:
MEDIUM TYPE: Diskett, 3.5 inch, 720kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1 or ASCII editors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid Synthetic DNA
                          391 gettategatacegtegaeetegaggggggee 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/377,383
FILING DATE: 25-JAN-1995
CLASSIFICATION NUBER: UF0971/1994
PRIOR APPLICATION NUBER: JP6971/1994
FILING DATE: 26-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Glenn J. Perry
REGISTRATION NUMBER: 286-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Glenn J. Perry
REGISTRATION NUMBER: 18458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 GGGGGGCCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202)822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 224 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-693-573-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: W
STATE:
                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 TCTATTTATTGCACGCCGCCGCCATGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 TCTATTTATTGCACGCGGCCGCCATGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAA 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 46; Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 91, Application US/09285479
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
ITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LUNG CANCER
FILE REFERENCE: 210121.455C3
CURRENT APPLICATION NUMBER: US/09/285,479
CURRENT APPLICATION NUMBER: US/09/285,479
NUMBER OF SEQ ID NOS: 172
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 47.7%; Score 70.6; DB 46; Best Local Similarity 84.9%; Pred. No. 1.6e-13; Matches 79; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 47.7%; Score 70.6; DB 43 Best Local Similarity 84.9%; Pred. No. 1.6e-13; Matches 79; Conservative 0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 GCTTATCGATACCGTCGACCTCGAGGGGGGCCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        391 gcttatcgataccgtcgacctcgagggggggcc 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 GCTTATCGATACCGTCGACCTCGAGGGGGGGCC 115
      ö
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      占
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                            þ
                                                                                                                                                                                                                                                                                                                                                                                       ь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ပဲ
                                                                                                                                                                                                                                                                                                                                                                                       ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(858)
; OTHER INFORMATION: n - A,T,C or G
US-09-285-479-91
                                                                                                                                                                                                                                                                                                                                                                                       ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (809)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                           LOCATION: (801)
OTHER INFORMATION: Where n is a,
                                                                                                                              n is
                                                                                                                                                                                                                                                                                                                                                   LOCATION: (804)
OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n 1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (820)
COTHER INFORMATION: Where n is
US-09-221-107-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Where
OTHER INFORMATION: Where
                                                                                                                           OTHER INFORMATION: Where
                                                                                                                                                     FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified_base
LOCATION: (817)
                                                               NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-09-285-479-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 91
LENGTH: 858
                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ģ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
```

Nuc1

ö

Gaps

ö

Indels

Length 224;

```
48 GGTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 121, Application US/08496841

GENERAL INFORMATION:
APPLICANT: St. George-Hyslop, Peter
APPLICANT: Rommens, Johanna M.
APPLICANT: Fraser, Paul E.
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSES: Testa, Hurwitz & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841 FILING DATE: 28-10N-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
NAME: TWOMMEY, Michael J
REGISTRATION NUMBER: 38349
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
46.2%; Score 68.4; DB 15;
Best Local Similarity 87.2%; Pred. No. 8.8e-13;
Matches 75; Conservative 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Testa, Hurwitz & Thibeault
High Street Tower - 125 High Street
FILING DATE: 28-APR-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 GGGGGCCTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 GGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: TWOMMEY, MICHAEL J
REGISTRATION UNDRER: 38,349
REFERENCE/DOCKET UNDRER: CAN-(
TELECOMMUNICATION INFORMATION:
TELEFAM: (617) 248-7000
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-431-048A-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 12. SEQUENCE CHARACTESISICS: LENGTH: 793 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: High StreCITY: Boston STATE: Massachuse COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-496-841-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-496-841-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 121. Application US/08431048A

GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASEN, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT, LLP
STREET: 125 High Street
CITY: BOSTON
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                               COUNTY: USA

ZIP: 20005-3918

COMPUTER READBLE FORM:
MEDIUW TYPE: DISKette, 3.5 inch, 720Kb storage COMPUTER: IBM PC/XT/AT compatibles OFFAMING SYSTEM: MS-DOS SOFTWARS: WORDFREECT 5.1 OF ASCII editors SOFTWARS: WORDFREECT 5.1 OF ASCII editors APPLICATION NUMBER: US/08/693,573
FILING DATE: US/08/693,573
PRIOR APPLICATION NUMBER: US/08/693,573
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: DF6971/1994
FILING DATE: 25-JAN-1995
ATORNEY/AGENT INFORMATION: NAME: Thomas G. Wiseman REGISTRATION NUMBER: 35046
FILING APPLICATION NUMBER: 35046
FILING SAEUTON NUMBER: 25-JAN-1994
ATORNEY/AGENT INFORMATION: TELEPHONE: (202)861-3000
TELEPHONE: (202)861-3000
TELEPHONE: (202)862-0944
TELETAN: (202)882-0944
TELETAN: G. DATE TO COSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
46.9%; Score 69.4; DB 18;
Best Local Similarity 87.4%; Pred. No. 2.9e-13;
Matches 76; Conservative 0; Mismatches 11;
                           STREET: Ninth Floor, 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: Other nucleic acid Synthetic DNA US-08-693-573-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GGGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 GGGGGGCCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EBNGTH: 224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                         CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-431-048A-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

ö

Indels

Length 793;

```
RESULT 14
US-09-124-523-121/c
                                                                                                                                                                                                      COUNTRY: UZIP: 07090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 GGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                  48 GGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                         119 GGGGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 60
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 46.2%; Score 68.4; DB 17; Length 793; Best Local Similarity 87.2%; Pred. No. 8.8e-13; Matches 75; Conservative 0; Mismatches 11; Indels 0;
        Length 793;
                                                                                                                                                                                                                                                         RESULT 12
US-08-509-159-121/C
Sequence 121, Application US/08509359
Sequence 121, Application US/08509359
Sequence 121, Application US/08509359
Sequence 121, Application US/08509359
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMENS, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTE RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPPLICATION NUMBER: US/08/509,359
FILING DATE: 31-JUL-1995
CLASSIFICATION: 800
      Score 68.4; DB 16;
Pred. No. 8.8e-13;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Testa, Hurwitz & Thibeault
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 13
US-08-509-359B-121/c
; Sequence 121, Application US/08509359B
                                                                                                                                                                 108 GGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 GGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                     59 GGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 GGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7362
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Twomey, Michael J
REGISTRATION NUMBER: 38349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-509-359-121
        46.28;
87.28;
Query Match
Best Local Similarity 87.29
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: High Street TO CITY: Boston STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                      ò
                                                                                                                         g
                                                                                                                                                                   ò
                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
48 GGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.2%; Score 68.4; DB 17; Length 793; 87.2%; Pred. No. 8.8e-13; tive 0; Mismatches 11; Indels 0.
                 APPLICANT: ROWMENS, JOHNNA M
APPLICANT: ROWMENS, JOHNNA M
APPLICANT: RASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSES: LEWRER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
STREET: 600 South Avenue West
CITY: Westfield
STATE: New Jersey
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 121, Application US/09124523
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMNENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: MICROSOft WORDS. DOS OFFWARE: MICROSOft Word, Version 6.0c CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/509,359B
FILING DATE: 31-JUL-95
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Palisi, Thomas M.
REGISTRATION NUMBER: 36629
TELECOMMUNICATION INFORMATION:
TELEPAN: (908) 654-7866
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 Jase Pairs
TENGTH: 793 Jase Pairs
TENGTH: 793 Jase Pairs
TENGTH: 793 Jase Pairs
TENGTH: 793 Jase Pairs
PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 GGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 GGGGGCCCGGTACCCAGCTTTGTT 34
ST. GEORGE-HYSLOP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
US-08-509-359B-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 87.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
```

ö

Length 793; Indels

```
48 GGTGGATCCCCCGGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                                                                                                                                                                                   Score 68.4; DB 40;
Pred. No. 8.8e-13;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: May 30, 2000, 09:48:31 Job time: 60181 sec
                                                                                                                                                                                                                                                                                                              108 GGGGGCCTAACTAACTAATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                            GGGGGCCCGGTACCCAGCTTTTGTT
                                       TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-124-698-121
                                                                                                                                           Query Match
Best Local Similarity 87.2%;
Matches 75; Conservative
  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 GGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GE-09-124-698-121/c
| Sequence 111, Application US/09124698
| GENERAL INFORMATION:
| APPLICANT: ST. GEORGE-HYSLOP, PETER H
| APPLICANT: ROMMENS, JOHANNA M
| APPLICANT: RASER, PAUL E
| TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
| UNUMERS OF SEQUENCES: 183
| CORRESPONDENCE ADDRESS:
| ADDRESSER: TESTA, HURWITZ & THIBEAULT
| STREET: High Street Tower - 125 High Street
| COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.

ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
46.2%; Score 68.4; DB 40;
Best Local Similarity 87.2%; Pred. No. 8.8e-13;
Matches 75; Conservative 0; Mismatches 11;
                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELEPHONE: (617) 248-7100
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: PICHOFY, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 121:
SECOURCE CHARACTERISTICS:
LENGTH: 793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 GGGGGCCTAACTAACTATTTTGTT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 GGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) US-09-124-523-121
                                                                                                                                                                                                                                                                                                                      LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

74 (A)			1.3 1.3			4	
			**************************************				4.4
,							
i g Mari							,
			•				
P.							
(Ž	as .						
1 3 3							
		÷					ŧ
į.		•					
ř				<u>.</u>			
i.							
			4				
i la			The state of the s				
<b>k</b>							3
)			15 to		• •	• .	
		· · · · · · · · · · · · · · · · · · ·		•	1		Vi
					1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1		t e
Ĭ				•			
<b>*</b>	manufacture of the second			1 	·		
1.7				•			2
<b>k</b>				i de la companya de La companya de la co			
<b>8</b>		•		. *		₹	
	e je sektori i najeta i najet						
•	경화 (1997年) 경영 (1997年) 1987년 - 李明朝 (1997年)					4	
					•		
					*		
		1.			j		
		•	**				of .
		Maria de Mar					
*							
*							<b>.</b> 
				y.		: £	*
r. Ç.				e y		1	
							2
			14 S	* •			
MA.		*	1.2.2.4. 22.4.2.4			av.	
4				*			

gb_est25:*
gb_est27:*
gb_est27:*
gb_est28:*
gb_est28:*
em_est29:*
em_est21:*

```
May 29, 2000, 21:13:15 ; Search time 2192.43 Seconds (without alignments) 273.613 Million cell updates/sec
                                                                              US-08-935-377-7
148
1 GGCCAAAAATTGAAAACTA......TTGTTTTGTGGGCCCGGCC 148
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                  4857316 segs, 2026611650 residues
                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                    OM nucleic - nucleic search, using sw model
                                                                                                           IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                  em_est11:*
em_est12:*
em_est13:*
                                                                                                                                                                                                                                                                                                                                                            em_est19:*
gb_est1:*
                                                                                                                                                                                                                                                                                                                                                                                                          gb_est6:*
gb_est7:*
gb_est8:*
gb_est9:*
gb_est10:*
gb_est111:*
                                                                                                                                                                                                                                                                                                                        em_est14:*
em_est15:*
em_est16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est14:*
gb_est15:*
                                                                                                                                                                                                                                                                                                                                               em_est17:*
em_est18:*
                                                                                                                                                                                                                                                                                           em_est10:*
                                                                                                                                                                                                                                                                                                                                                                            gb_est2:*
gb_est3:*
gb_est4:*
gb_est5:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est13:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est17:*
                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est21:
                                                                                                                                                                                                                          em_est1::
em_est2::
em_est4::
em_est5::
em_est5::
em_est7::
em_est8::
em_est8::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est20:
                                                                                                                                                                                                                    EST: *
                                                                               Title:
Perfect score:
                                                                                                           Scoring table:
                                                                                                                                                                                                                    Database :
```

Searched:

Sequence:

Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

gb_gss13:*
gb_gss14:*
gb_gss15:*
gb_gss15:*

em_gss8:* gb_gss11:* gb_gss10:* em_gss9:*

gb_gss7:* gb_gss8:* gb_gss9:* em_gss7:*

gb_gss5:*
gb_gss6:*
em_gss5:*

gb_gss3:* gb_gss4:* em_gss1:* em_gss2:*

em_gss3: em_gss4:

em_gss10: em_gss11: em_gss12: gb_gss12:

SUMMARIES

Result No.

Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA	Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search.html. Seq primer: M13-21 Class: BAC ends. Location/Qualifiers 1. 682 /organism."Homo sapiens" /db_xref="taxon:9606" /clone="2301L23" /clone="2301L23" /clone="2301L23"	/sex="Made"   /sex="Made"   /sex="Made"   /sex="Made"   /note="Yoctor: pBeloBAC11; Site_1: HindIII; Site_2: HindIII   156 a 187 c 187 g 151 t 1 others ORIGIN   47.6%; Score 70.4; DB 96; Length 682; Best Local Similarity 92.5%; Pred. No. 2e-13; Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0; Matches 74; Conservative 0; Mismatches 6; Indels 0; Gaps 0; HINIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 80 Qy 107 Db 20 RESULT AQ0091677	Quomic survey sequence.  AQ009167.1 G1:3128599  AQ009167.1 G1:3128599  Homo saplens  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; M  Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 608)  Adams, M.D., Rounsley,S.D., Field,C.E., Bass,S., Linhe  Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Ki  Shizuya,H., Simon,M. and Venter,J.C.  Use of a human BAC End Sequence Database for Sequence	Building AL Unpublished (1997) Other_GSSS: CIT-HSP-2281N13.TR.1 CIT-HSP-2281N13.TF CIT-HSP-2281N13.TR CIT-HSP-2281N13.TR Contact: Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0200 Fax: 301 838 0200	Clones are available from Research Genetics (Info@resgen.com). BAC end search page:     http://www.tigr.org/tdb/humgen/bac_end_search.html     seq primer: Mi3-21;     Class: BAC ends.     Location/Qualifiers     source     1. 608
Description	AQ074693 CIT-HSP-2 B69688 CITJ-HSP-2 B69688 CITJ-HSP-2 B54292 CIT-HSP-201 AU037147 AU037147 B95279 CIT-HSP-201 B00294 CIT-HSP-204 AQ013255 CIT-HSP-2 AQ041198 CIT-HSP-2 T48593 Ph6f4 19/1T AA052885 T3551 B10 B74162 CIT-HSP-202 AQ014512 CIT-HSP-202 AQ014512 CIT-HSP-202 AQ014512 CIT-HSP-202 AQ014512 CIT-HSP-202	AQ012629 CIT-HSP-2 AQ012216 CIT-HSP-2 AQ012212 CIT-HSP-2 AQ001223 CIT-HSP-2 B04363 CIT-HSP-202 B70299 CIT-HSP-202 AQ016737 CIT-HSP-204 B80296 CIT-HSP-204 AQ091953 CIT-HSP-204 AQ091953 CIT-HSP-204 AQ074695 CIT-HSP-2	AQU145.19 B72088 CIT978SK-13 B26269 F10B5TF IGF AQ012365 CITHSP-2 T26395 AB161A4F IN AL239372 SWOVABCAP U68746 Riftia pach AQ003238 RPCIII-19 B58695 CIT-HSP-201 AA752115 96B80066 AI058116 SWAMCAC15	B65391 CTT-HSP-202 B002418 CPGR0359A A0023564 CPGR0482A A0023547 CPGR051A A0024029 CIT-HSP-2 A0023674 CPGR0007B	GSS 20-AUG-1998 genomic clone 2301L23, Vertebrata; Mammalia; ae; HOmo.	's,S., Linher,K., Golden,K., Shizuya,H., Simon,M. and Database for Sequence-Ready
Length DB ID	6 682 96 AQ074693 2 6 608 96 AQ09167 8 128 84 B89688 108 84 B54292 5 141 44 AU037147 5 144 84 B80279 5 144 84 B80279 5 15 96 AQ013255 5 175 96 AQ013255 5 275 27 AAC8285 5 386 84 B7462 5 46 96 AQ014512	55 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	541 1334 1334 1334 1032 100 100 100 100 100 100 100 100 100 10	444 4744 4744 4744 4744 4744 4744 4744	DNA SP Homo sapiens Gata; Craniata;	1 (bases 1 to 682) Adams, M.D., Rounsley, S.D., Zhao, S., Bass Berry, K., Granger, D., Suh, E., Wible, C., Venter, J.C. Venter, J.C. When a random human BAC End Sequence 1 Map Building Unpublished (1998) Contact: Mark Adams
Query re Match			444444mmmmm4474700000000000000000000000	556 556 556 566 566 566 566 567 567 567	AQ074693 CIT-HSP- genomic AQ074693 AQ074693 GSS. Human. Homo sap Eukaryot Eutheria	1 (bas Adams,M Berry,K Venter, Use of Map Bui Unpubli

υυ

υυυ

00000

RESULT 1 AQ074693/c LOCUS DEFINITION

υo

υυυ υ

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

```
Best Local Similarity 97.2
Matches 69; Conservative
                                                                                                                      107 GGGGGGCCTA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGGGCC 1.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 a
                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92
                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                     음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L Unpublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Fibroblast"
/cell_type="Fibroblast"
/note="Vector: pBACI08L; Site_1: HindIII; Site_2: HindIII;
/note="Wector: pBACIAbrax A"
138 c 147 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B69688 528 bp DNA GSS 18-JUN-1998
CIT978SK-A-448E10.TVC CIT978SK Homo sapiens genomic clone A-448E10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 528)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Kim,U.-J.,
Shizuya,H., Simon,M. and Venter,J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                          47 IGGIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:1147360"
/db_xref="GDB:1147360"
/db_xref="GDB:1147360"
/clone="2281N13"
/clone_lib="CIT-HSP"
/csh="ker="Sperm"
/cell_type="Sperm"
/note="Vector: pBelobAc11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                     Length 608;
                                                                                                                                                                                                                      Query Match 46.2%; Score 68.4; DB 96; Length (Best Local Similarity 98.6%; Pred. No. 9.3e-13; Matches 69; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic survey sequence.
B69688
B69688.1 GI:2708912
                                                                                                                                                          164 c
                                                                                                                                        HindIII"
                                                                                                                                                                                                                                                                                                                                                             107 GGGGGGGCCT 116
                                                                                                                                                          141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
B69688/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                            õ
                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                             g
```

```
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutherite; Primates; Catarrhini; Hominidae; Homo.

Eutherite; Primates; Catarrhini; Hominidae; Homo.

Eutherite; Primates; Catarrhini; Hominidae; Homo.

3 Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,

Golden,K., Barry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M. and Venter,J.G.

Building

AL Dipublished (1997)

Contact: Mark Adams

Eutherite for Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Seq primer: Mi3 Reverse

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                 B54292 108 bp DNA GSS 20-JUN-1998 CIT-HSP-2017M1.TR CIT-HSP Homo sapiens genomic clone 2017M1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67.4; DB 84; Length 108;
Pred. No. 1.5e-12;
0; Mismatches 1; Indels 0;
97.2%; Pred. No. 1.4e-12;
tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .108
/organism-"Homo sapiens"
/db_xref="GDB:7044003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="2017M1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.6%;
Matches 68; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                     B54292.1 GI:2608626 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HindIII"
```

RESULT AU037147

DB 84; Length 528;

Score 67.8;

Query Match

```
Admo Sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutaryota; Metazoa; Catarrhini; Hominidae; Homo.

E Utbaces 1 to 144)

S Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Barry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)

U Unpublished (1998)

Other_GSSS: CIT-HSP-2045D19.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadamsetigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: MI3 Reverse
Class: BAC ends.
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BB0294 144 bp DNA GSS 24-OCT-1998 CIT-HSP-2045D19.TR CIT-HSP Homo sapiens genomic clone 2045D19, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                     /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 98.6%; Pred. No. 1.6e-12;
Matches 68; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                               35 t
                                                                                                                                                                                       1. .141
/organism="Homo sapiens"
/db_xxef="GDB:710398"
/db_xref="taxon:9606"
/clone="2172N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 144
/organism="Homo sapiens"
/db_xref="GDB:7054558"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                              /clone_lib="CIT-HSP"
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                   41 g
                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:2867317
                                                                                                                                                                                                                                                                                                                                                                                                      41 c
                                                                                                                                                                                                                                                                                                                                                                              HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B80294
B80294.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 GGGGGGCC 7
                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
B80294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhini; Hominidae; Homo.

E (bases 1 to 141)
Adams.M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)
Upublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                   Dictyostellum discoideum.
Dictyostellum discoideum
Dictyostellum discoideum
Dictyostellum discoideum
Dictyostellum discoideum
Dictyostellida, Dictyostellum.
Dictyostellum, Dictyostellum.
Worlo, T., Urushihara, H., Salto, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yalto, T., Takenoto, K., Yasukawa, H., Yoshino, R., Mitz, B.N., Pi, N., Salto, T., Takenoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochidai, H. and Tanaka, Y.
The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
               AU037147 141 bp mRNA EST 29-MAR-1999 AU037147 Dictyostellum discoideum SS (H.Urushihara) Dictyostellum discoideum cDNA clone SSB532, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B95279 141 bp DNA GSS 26-JUN-199
CIT-HSP-2172N2.TF CIT-HSP HOMO SAPIENS GENOMIC CLONE 2172N2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-3-10 Ten-nodal Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                                                                                                                                                                                On Jan 19, 1998 this sequence version replaced g1:2153012.
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .141
/organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67.4; DB 44;
Pred. No. 1.6e-12;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="AX4"
/db_xref="taxon:44689"
/clone="SSB532"
                                                                                                                                                                                                                                                                                                                                         DNA Res. 5 (6), 335-340 (1998)
99156227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="slug"
40 c 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
895279
895279.1 GI:2977616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.5%;
                                                                                                     AU037147.1 GI:3983900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGGGCC 135
                                                                                                                                                                                                                                                                                                                                   development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
COMMENT
                         LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                     ORGANISM
                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
B95279/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                              TITLE
```

ð 엄 ò 8

```
131 GGGGGGCC 139
                                                                        107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GGGGGGCC 115
                                                                                                      43 GGGGGGCC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43
                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS DEFINITION
                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
COMMENT
                                                                                                                                                                  AQ041198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
T48593
                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                   RESULT
                                            g
                                                                          á
                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota: Metazoa, Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169)

Sadams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Lu Onpublished (1998)

Other_GSSs: CIT-HSP-229G22.TR

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3-21
Class: BAC ends.
                                                                                                                                                                                                          47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                             AQ013255 169 bp DNA GSS 06-JUN-1998
CIT-HSP-2299C22.TF CIT-HSP Homo sapiens genomic clone 2299C22,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
/clone="2045D19"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 67.4; DB 96; Length 169;
Pred. No. 1.7e-12;
0; Mismatches 1; Indels 0
                                                                                                                                                   Length 144;
                                                                                                                                                                              1; Indels
                                                                                                                                               Score 67.4; DB 84;
Pred. No. 1.6e-12;
                                                                                                                                                                              0; Mismatches
                                                                                        56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .169
/organism="Homo sapiens"
/db_xref="GDB:7154018"
/db_xref="taxon:9606"
/clone="2299622"
/clone="lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                      41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
                                                                                                                                                                                                                                                                                                                                                                                                                     AQ013255
AQ013255.1 GI:3185820
                                                                                                                                               45.5%;
98.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.5%;
                                                                                        43 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47 C
                                                                                                                                                                              68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 98.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                               Best Local Similarity
Matches 68; Conser
                                                                                                                                                                                                                                                                                        128 GGGGGGCC 136
                                                                                                                                                                                                                                                                   107 GGGGGGGCC 115
                                                                                           ಡ
                                                                                        34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                         AQ013255/c
LOCUS
                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                             ô
```

```
Homo sapiens
Eutheria; Matazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 175)
Golden, X., Barry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.G.

Building (1988)
Lunbublished (1998)
Contact: Mark Adams
Eutheria; Mark Adams
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T48593 259 bp mRNA EST 02-FEB-1995 ph6f4_19/1TV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph5f4_19/1TV, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                                                                                                                                                                                                                                                                                                                                                                                        AQ041198 175 bp DNA GSS 14-JUL-1998 CIT-HSP-2335D21.TR CIT-HSP Homo sapiens genomic clone 2335D21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 TGGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 106
                                  103 TAGTGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lb="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.5%; Score 67.4; DB 96; Best Local Similarity 98.6%; Pred. No. 1.7e-12; Matches 68; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2335D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ041198
AQ041198.1 GI:3310469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HindIII"
```

SOURCE

```
/db.xruf="Lookstream form of serodeme ILTatl.1"
/db.xruf="Laxon:5702"
/clone_lib="Bloodstream form of serodeme ILTatl.1"
/clone_lib="Bloodstream form of white an iched mRNA
/clone_nonate from different developmental stages of T.b.Drucei
prepared from different developmental stages of T.b.Drucei
by reverse transcription followed by PCR amplification
using mini-exon and oligo(dT) primers. The CDNA generated
were utilized in RADES-PCR coupled with differential
hybridisations to identify differentially expressed mRNA
transcripts. The products which showed to.be
differentially expressed were cloned pGEM -T vector.
These differentially expressed mRNA transcripts were (are
being) sequenced to generate differentially expressed
sequence tags."

56.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
Other_GSSS: CIT-HSP-2028NI.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research Genetics (Info@tesgen.com). BAC
Clones are available from Research Genetics (Info@tesgen.com). BAC
Glones are available from Research Genetics (Info@tesgen.com). BAC
Glones are available from Research Genetics (Info@tesgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Building a random bac End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 IGGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGA 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B74162 386 bp DNA GSS 24-OCT-1998
CIT-HSP-2028NI.TF CIT-HSP Homo sapiens genomic clone 2028NI,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67.4; DB 27; Length 275; Pred. No. 1.8e-12; 0; Mismatches 1; Indels 0
                                                                                                                           /organism="Trypanosoma brucei brucei"/strain="clone A4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 386
/organism="Homo sapiens"
/db_xref="GDB:7048251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 9
                                                                               Location/Qualifiers
Fax: 254 2 631 499
Email: a.osanya@cgnet.com
Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 98.6%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B74162
B74162.1 GI:2769849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
B74162/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                    Contact: Sverdlov ED
Structure and Function of Human Genes
Shemyakin Institute of Bioorganic Chemistry
Shemyakin Institute of Bioorganic Chemistry
16/10 Miklukho-Maklaya, Moscow, 117871, Russia

16/10 Miklukho-Maklaya, Moscow, 117871, Russia

17/10 Miklukho-Maklaya, Moscow, 117871, Russia

17/10 Miklukho-Maklaya, Sapiens
17/10 Location/Qualifiers
17/10 Miklukho-Maklaya
17/10 Location/Qualifiers
17/10 Location/Qualifiers
17/10 Miklukho-Maklaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 259)

1 vhogradova_T.V., Lebedev_Y.B., Kopantzev,E.P., Wagner,L.L., Volik_S.V., Ermolaeva,O.D., Lavrentyeva,I., Monastyrskaya,G.S. and sverdlov,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA052885 275 bp mRNA EST 13-SEP-1996
T3551 Bloodstream form of serodeme ILTatl.1 Trypanosoma brucei
brucei cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 275)
Osanya,A., Murphy,N.B. and Pelle,R.
Trypanosoma brucei brucei cDNAs
Unpublished (1996)
On Nov 29, 1993 this sequence version replaced g1:637578.
Contact: Osanya A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67.4; DB 20; Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  International Livestock Research Institute
Box 30709, Nairobi, Kenya
Tel: 254 2 630 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.8e-12;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                       Outward Alu-primed hncDNA library Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma brucei brucei. Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA052885
AA052885.1 GI:1543898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45.5%;
                                            GI:642793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 68; Conservat
                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 GGGGGGCC 122
                    T48593
T48593.1
                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA052885
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                      REFERENCE
AUTHORS
                    ACCESSION
                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
```

g ö

ö

; 0

```
B65534.1 GI:2639512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 GGGGGGGCC 115
                                                                              107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 GGGGGGGC 16
                                                                                                41 GGGGGGGCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ012629
                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
AQ012629
LOCUS
                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                      B65534/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                   윱
                                                                             à
                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   쉽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 462)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

N. Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Email: mdadams@tign.org
Clones are availabe from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                       AQ014512 462 bp DNA GSS 06-JUN-1998 CIT-HSP-2300D21.TF CIT-HSP Homo sapiens genomic clone 2300D21, genomic survey sequence.
AQ014512.1 GI:3184839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
/db_xref="taxon:9606"
/clone="2028N1"
/clone_lib="CIT-HSP"
/ssy="walle"
/cell_type="Sperm"
/cell_type="Sperm"
/cell_type="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                      45.5%; Score 67.4; DB 84; Length 386; 98.6%; Pred. No. 1.9e-12; Live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
45.5%; Score 67.4; DB 96;
Best Local Similarity 98.6%; Pred. No. 1.9e-12;
Matches 68; Conservative 0; Mismatches 1;
                                                                                                             98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 462
/organism="Homo sapiens"
/db_xref="GDB:7154425"
/db_xref="taxon:9606"
/clone="2300D21"
/clone_11b="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Socation/Qualifiers
                                                                                                        109 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 c
                                                                                                              98 c
                                                                                                                                                                                        Best_Local Similarity 98.69
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HindIII"
                                                                                              "IIIDUIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                 107 GGGGGGGCC 115
                                                                                                                                                                                                                                                                                                                  24 GGGGGGGCC 16
                                                                                                                Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                             81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nman.
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
AQ014512/c
                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                  g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Other GSSs: CIT-HSP-2022D24.TR
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mddadms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B65534 51-JUN-1998 CIT-HSP-2022D24.TF CIT-HSP Homo sapiens genomic clone 2022D24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.5%; Score 67.4; DB 84; Length 519; Best Local Similarity 98.6%; Pred. No. 2e-12; Matches 68; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 519
'Organism" Homo saplens"
/db_xref="GDB:045730"
/db_xref="taxon:9606"
/clone="2022D24"
/clone="ib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
```

DEFINITION

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                         /clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
139 c 125 g 129 t
CIT-HSP-2299F1.TR CIT-HSP Homo sapiens genomic clone 2299F1, genomic survey sequence. AQ012629 GI:3185194
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 45.5%; Score 67.4; DB 96; Length 547; Best Local Similarity 98.6%; Pred. No. 2e-12; Matches 68; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:7154069"
/db_xref="taxon:9606"
/clone="2299F1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 GGGGGGCC 141
                                                                                                                                                                                                                                                                                                                                                       154
                                              human.
                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                REFERENCE
AUTHORS
                                                                                                                                    JOURNAL
COMMENT
                                                                                                                                                                                                                                                      FEATURES
                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                            δλ
```

Search completed: May 29, 2000, 21:13:16 Job time: 36515 sec

١

Run on:

```
U14122 Cloning vec X44281 Sequence 9 X52326 pBluescript X52339 pBluescript X52329 pBluescript L08784 Bluescript L08784 Bluescript L08784 Bluescript L08784 Bluescript L08784 Bluescript L08785 Cloning vec U3435 Yeast integ U03435 Yeast integ U03435 Yeast centr U03440 Yeast centr U03440 Yeast centr U23751 Cloning vec U34687 Yeast integ U25059 Cloning vec U3442 Yeast centr U23751 Cloning vec U0343 Yeast integ U35059 Cloning vec U0343 Yeast centr U23751 Cloning vec U0343 Yeast centr U35059 Cloning vec U0343 Yeast Control W341 Yeast Cloning vec U03441 Yeast Cloning vec W22847 Cloning vec W22847 Cloning vec W22847 Cloning vec W25324 pBluescript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X52325 pBluescript
X52330 pBluescript
X5238 pBluescript
L08787 BlueScribe
L08786 BlueScribe
L08787 BlueScribe
U08787 BlueScribe
U08787 BlueScribe
U08785 BlueScribe
U08785 Plasmid pBS
U35132 plasmid pBS
U35132 Plasmid pBS
AF139061 Blnary ve
                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                            CVU14122
A44281
ARBLKSM
ARBLKSK
ARBLZKSM
ARBLZKSP
ARBLZKSP
SYNBLKSPV
SYNBLKSPV
SYNBLKSPV
SYNBLKSPV
SYNBLKSPV
SYNBLKSPV
FR3304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARBL2SKM
ARBL2SKP
SYNBLDKPV
SYNBLSKMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASAJ5323
SYNPGR8V
AF015771
SYNPLKRA
SYNPLKRB
ARBLSKM
ARBLSKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CVE7829
                                                                                                                                                                                                                                                                                             Query
Match Length DB
                                                                                                                     gb_htg9: *
gb_htg10: *
gb_htg11: *
gb_htg12: *
gb_htg13: *
gb_htg13: *
gb_htg6:*
gb_htg7:*
em_htg1:*
em_htg2:*
em_htg3:*
                                                                 em_hum5:*
gb_p13:*
gb_pr5:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_htg8:
                                                                                                                                                                                                                                                                                                                                  73.6
                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                             Result
                                                                                                                                                                                                                                                                                                          8
8
                                                                                       May 29, 2000, 21:35:34 ; Search time 1214.87 Seconds (without alignments) 934.219 Million cell updates/sec
                                                                                                                                                            149
1 GGCCAAAAATTGAAAACTA......TTGTTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                  1765538
             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                                                                                                                                        882769 seqs, 3808571567 residues
                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                   - nucleic search, using sw model
                                                                                                                                                                                                 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                               US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_hum1:*
em_hum2:*
em_in:*
                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_htg2:*
gb_in1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yb_htg1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_pr2:*
gb_pr3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_ro:*
gb_sts:*
gb_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_un:*
gb_vi:*
em_fun:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_or:*
em_ov:*
em_ph:*
em_pl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_ba2:*
em_hum3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_in2:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         em_bal:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_om: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_sts:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_v1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_pr1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_ov: *
gb_pat:
gb_ph: *
gb_pl1:
                                                                                                                                                                                                                                                                                                                                                                                        GenEmbl:*
                                                                                                                                             Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                  Total number of
                                                                                                                                                                                                 Scoring table:
                                                                   OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                        Database :
                                                                                                                                                                                                                                         Searched:
```

ô

Gaps 64

; 0

07-MAR-1997

DEFINITION ACCESSION VERSION KEYWORDS

CVU14122/c

RESULT

ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE REFERENCE

TITLE JOURNAL

AUTHORS

```
unclassified.

1 bases 1 to 259)

Chandley, A.C., Kun, M., Sharkey, A.M., Hargreave, T.B. and Cooke, H.J. AZOOSPERMIA IDENTIFICATION AND TREATMENT
AZOOSPERMIA IDENTIFICATION AND TREATMENT
MEDICAL RES COUNCIL (6)
Other publication AU 7947794 950508.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thomas, E.A.

Direct Sundission

Submitted (2007-FEB-1990) Thomas B.A., Stratagene Clonin Systems,
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
2 (bases 1 to 2958)

Short, J.M., Fernandez, J.M., Sorge, J.A. and Huse, W.D.
Short, J.M., a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARBLKSM 2958 bp DNA circular SYN 10-MAY-1995
pBluescript KS(-) vector DNA, phagemid excised from lambda ZAP.
X52326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43 GCCATGAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGAC 102
                                                                  5 AAAAATIGAAAAACIAGAICIAIITATIGCACGCGGCCGCCAIGAGIGGAICCCCCGGGC
                                                                                                                   65 TGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCC 116
                                                                                                                                      Score 71.2; DB 5; Length 259;
Pred. No. 2.6e-12;
0; Mismatches 13; Indels
Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        excision properties ... Nucleic Acids Res. 16 (15), 7583-7600 (1988) 88319944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"unidentified"
/organism-"taxon:32644"
/clone_lib-"wou'sE GENOMIC LIBRARY"
/clone="M3.2"
                                                                                                                                                                                                                                                                  PAT
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ų
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 CTCGAGGGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                            A44281 259 bp DNA
Sequence 9 from Patent W09511300.
A44281
A44281.1 GI:2299115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (bases 1 to 2958)
Alting-Mees, M.A. and Short, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 g
  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.8%;
illarity 85.9%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X52326.1 GI:58064
  Conservative
                                                                                                                                                                                                                                                                                                                                                                       unidentified
unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29
    88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                              RESULT 2
A44281/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
ARBLKSM
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                         음
                                                                                 g
                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / ALD XXEOF = 0.01 : 5.314.03 ...
/ ALD XXEOF = 0.01 : 5.314.03 ...
/ LT ans lation = WHEPLLPARASVAEFDNSLSIVGKAVFPYAADQLHNLIKFTQST
/ LT ans lation = WHEPLLPARASVAEFDNSLSIVGKAVFPYAADQLHNLIKFTQST
ELOVNVQVESSVYEDQFEELIDDLIKLYNNGINEVILDEDLEERVVQRYPGARYIYRT
INDROLFTEYELSEDVKKFPVSEILLASITTORPDGLFTTUADSSNYSIGIVYSSK
KSIPEATROFCYYQSRRHGLMYKGARGARGARGALLELDCDEDLKFVVEQTGGLYGSK
KSKEDIAWECADLFYFANGARTAWDRSSYTRRIFDDEVLLMAKIREEADELAEA
RSKEDIAWECADLFYFANGARYGYTLDEVENLDMKSLKVTRRKGDAKPGYTKEQP
KEESKRKEVPEGGRIELCKIDVSKASYGEIEDALGREPOTTORTORYRGU
GDRAALBLITAKFDGVALKTPVLEAFFFEELMQLFDNVKRIDLSIDNVRKFHEAQLAE
TLQVFTCPGYVCSRFARFIEKVGLYTEGGFALLPESTSIMGGYPARAYGGETYPRAGDER
KKDGTLFFEVIYVAHKVGAKCIVLAGGAQAVAMAXGTETYPRAGGETTYPGONTTETATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
IELDLNSGKILESFRPERFPPMSTFRYLLGGAVLSRIDGGBQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSATTMSDNTAANLLLTTIGGRKELTAFLHNMGDHVTRL
DRWEPELNEAIPNBEDTTMSDNTAANLLLTTIGGRKELTAFLHNMGDHVTRL
LIRSALPAGNFTAADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW" 1372 9 1484 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KMMVQNDTSALCSIDMPAGPSEVLVIADKYADPDFVVSDLLSQAEHGIDSQVĪLLAVD
MTDKELARIEDAVHNQAVQLPRVEIVRKCIAHSTILSVATYEQALEMSNQYAPEHLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OIENASYVDQVQHAGSVFVGAXSPESGGDYSSGINHTLPTYGYARQYSGVNTATFQKF
ITSQDVTPEGLKHIGQAVMDLAAVEGLDAHRNAVKVRMEKLGLI"
complement(4651. .5511)
                                                                                                                                                                                                                                                                                                                                                                       Gould, S.J.
Gould, S.J.

Gould, S.J.

Birect Submission
Submitted (29-AUG-1994) Stephen J. Gould, Neurogenetics, The
Kennedy Krieger Institute, 707 North Broadway, Baltimore, MD 21030,
USA.
                                                                                                                                                                                       Cloning vector psG935.
Cloning vector psG935
Cloning vector psG935
artificial sequence; vectors.
1 (bases 1 to 5639)
Crane, D.1. and Gould, S.J.
The Pichia pastoris HIS4 gene: nucleotide sequence, creation of a non-reverting his4 deletion mutant, and development of HIS4-based replicating and integrating plasmids
Curr. Genet. 26 (5-6), 443-450 (1994)
                                                                          CVUI4122 5639 bp DNA circular SYN 20-MAY-1995 Cloning vector pSG935, HIS4-based plasmid, complete sequence. UI4122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 73.6; DB 14; Length 5639; Pred. No. 6.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
/product="histidinol dehydrogenase"
/protein_id="AAA66991.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 5639
/organism="Cloning vector pSG935"
/plasmid="rpSG935"
/db_xref="taxon:36585"
/lab_host="richia pastoris"
833. 3361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"beta-lactamase"
/protein_id-"AAA66992.1"
/db_xref-"GI:537472"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.48;
78.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="HIS4"
833. 3361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      833. .3361
/gene="HIS4"
                                                                                                                                                     U14122.1 GI:537471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1473
```

source

FEATURES

gene

CDS

BASE COUNT ORIGIN

CDS

ö

Gaps

\$

misc_feature

BASE COUNT

ORIGIN

Matches 49

g ò 윱

source

TITLE JOURNAL MEDLINE

```
artificial sequence.

( pases 1 to 2961)

Thomas E.A.

Direct Submission

Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems, 11099 North Torney Pines Rd., La Jolla, CA 92037, USA

( Dases 1 to 2961)

Short, J.M., Fernandez, J.M., Sorge, J.A. and Huse, W.D.

Lambda Lash: a bacteriophage lambda expression vector with in vivo Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X5237.1 GI:58061
artificial sequence; cloning vector; expression vector; vector.
synthetic construct.
synthetic construct.
artificial sequence.
I (bases 1 to 2961)
Thomas, E.A.
Direct Submission
Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
                   686 AGTGGATCCCCCGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 745
                                                                                                                                                                                                                                                                                  cloning vector; expression vector; vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARBL2KSM 2961 bp DNA circular SYN 10-MAY-1995
pBluescript II KS(-) vector DNA, phagemid excised from lambda
ZAPII.
Score 70; DB 14; Length 2961;
Pred. No. 8e-12;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARBLZKSP 2961 bp DNA circular SYN pBluescript II KS(+) vector DNA, phagemid excised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. 2961
/organism="synthetic construct"
/db_xref="taxon:32630"
1. 2961
/note="phagemid pBluescriptII KS(-)"
/s a 758 c 735 g 762 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 (bases 1 to 2961)
Alting-Mees, M.A. and Short, J.M.
Paluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GGGGGCCTAACTAACTATTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.4%;
Matches 76; Conservative C
                                                                                                                                                                                                                                                                                artificial sequence;
                                                                                                                                                                                                                                                                                                      synthetic construct
synthetic construct
                                                                                                                                                                                                                                             X52329
X52329.1 GI:58060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88319944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARBL2KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZAPII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
DEFINITION
                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                   RESULT
ARBL2KSM
                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
ARBL2KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                   g
                                                        à
                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lampe, D.J., Grant, T.E. and Robertson, H.M.
Factors affecting transposition of the Himarl mariner transposon in
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems, 11099 North Torney Pines Rd., La Jolla, CA 92037, USA C bases 1 to 2958)
Short,J.W., Fernandez,J.W., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequence; cloning vector; expression vector; vector synthetic construct. synthetic construct
                                                                                                                                                                                                                                                                                                                                       circular SYN 11-JUN-1998
phagemid excised from lambda ZAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                      AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.0%; Score 70; DB 14; Length 2958; 88.4%; Pred. No. 8e-12; tive 0; Mismatches 10; Indels ...
                                                                                                                                                                                                                                             Score 70; DB 14; Length 2958;
Pred. No. 8e-12;
                                                                                                                                                                                                                                                                                0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                 /note="phagemid pBluescript KS(-)" 754 c 731 g 765 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KS(+)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .2958
/organism="synthetic construct"
/db_xref="taxon:32630"
                                                   Location/Qualifiers
1. .2958
/organism="synthetic construct"
/b.xref="taxon:32630"
1. .2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2958)
Alting-Mees, M.A. and Short, J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. 2958
/note-"phagemid pBluescript
/note 734 c 751 g 724 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics 149 (1), 179-187 (1998)
98250682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARBLKSP 2958 bp DNA
pBluescript KS(+) vector DNA,
X52331
X52331.1 GI:58065
                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGCCTAACTAACTTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                    ch 47.0%;
1 Similarity 88.4%;
76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            artificial sequence.
1 (bases 1 to 2958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas, E.A.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 76; Conserva
                                                                                                                                                                                                                                           Query Match
Best Local Similarity
```

DEFINITION

RESULT ARBLKSP

ACCESSION VERSION

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE JOURNAL

REFERENCE

REFERENCE AUTHORS TITLE

JOURNAL

ö

Gaps

ö

10-MAY-1995 from lambda

749

BASE COUNT

**Ouery Match** 

misc_feature

MEDLINE REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE

AUTHORS TITLE

JOURNAL MEDLINE

```
© ©
                                                                                                                                                                                                                                                                                                         3 458 5488-5943
460-624 236-400
626-645 1-20
653-760 108- 1 (c)
                                                                                                                                                                                                                                                                                                                                                                                                         448-2617
                                                                                                                                                                            VecBase(3):BlueM13m
                                                                                                                       KEYWORDS
CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYLINKER
                                                                                                                                                             #parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNBLKSPV
LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                               ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
2 (bases 1 to 2961)
Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacterlophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Obtained from VecBase 3.0
Unpublished (1991)
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Currator Program.
BlueScribe KS Minus - Cloning vector
BINESS BLUESCH
TITLE BlueScribe KS Minus - Cloning vector
DATE
28-JAN-1987
#sequence 04-MAR-1987
#sequence 04-MAR-1987
#sequence 01-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #journal Gene (1987) in press
#citation Sequence data from StrataGene
#comment sequence correction according to Stratagene COMMENT
Obtained from StrataGene on floppy disc.
Revised 02-FEB-1987 by F. Pfeiffer:
Revised 4 MAR-1987 to match revised sequence of PBR322
Revised 4 MAR-1987 to match sequence of pUC19 on request
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Stratagene
Polylinker region revised 03-APR-1987 according to Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 AGIGGAICCCCCGGGCTGCAGGAATICGAIAICAAGCTIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                          Score 70; DB 14; Length 2961;
Pred. No. 8e-12;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                         /note="phagemid pBluescriptII KS(+)" 738 c 755 g 721 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   circular SYN
                                                                              excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                 Location/Qualifiers
1. 2961
Action/Synthetic construct"
Ab_xref="taxon:32630"
1. 2961
                                                                                                                                 Alting-Mees, M.A. and Short, J.M.
Alting-Mees, M.A. and Short, J.M.
Mulling-mees, M.T. and Short, J.M.
Nucleic Acids Res. 17 (22), 9494 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYNBLKSMV 2964 bp DNA circu
BlueScribe KS Minus cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             746 GGGGGGCCGGTACCCAGCTTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 GGGGGCCTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic construct DNA. synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                               47.0%;
llarity 88.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             artificial sequence.
1 (bases 1 to 2964)
Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L08784
L08784.1 GI:310728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION VB007
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                    38319944
                                                                                                                                                                                                                                                                                                                                747
                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
SYNBLKSMV
                                                                                                                                                     AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                              AUTHORS
TITLE
                                                                                                                  MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                 JOURNAL
```

COCUS

ö 셤 à 셤

```
ö
The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lacZ region is on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KpnI-brail-Apal-Xhol-Sall-Clal-Hindill-EcoRV-EcoRI-Pstl-
Smal-BamHI-Spel-Xbal-Notl-Xmalll-BstXI-Sacil-Saci SELECTION
                                                                                                                                                                                                                                                        'vecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
VecSource(3):bGalKS, GenBank(50):PF1
#brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AGIGGAICCCCCGGGCTGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This vector contains the fl origin so that the minus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

47.0%; Score 70; DB 14; Length 2964;
Best Local Similarity 88.4%; Pred. No. 8e-12;
Matches 76; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #checksum 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 start of T7-RNA synthesis
774 (c) start of T3-RNA synthesis
1976-2764 789-1 (c) Ap-R; b-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 promoter
) BlueKS-polylinker
) T3 promoter
puCl9c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blueks-polylinker
T3 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                circular SYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       653- 760 108- 1 (c) BluekS-polylinke 772- 791 20- 1 (c) T3 promoter 755-1031 237- 1 (c) pUC19 1032-2964 2686- 754 (c) pUC19 Confilt (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conflict (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                 VecBase(3):BlueKSp, VecBase(3):BlueSKm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="synthetic construct"
/db_xref="taxon:32630"
/ 756 c 735 g 765 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I7 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                        phage fl
puc19c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phage fl
puci9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNBLKSPV 2964 bp DNA circ
BlueScribe KS Plus cloning vector.
L08785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #resistance Ap
#indicator beta-galactosidase
SUMMARY BlueKSm #length 2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Features of BlueKSm (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                               Features of BlueKSm (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
5488-5943
449- 285 (c)
```

SOURCE

```
/db_xxeef="G1:1345434"
/translation="MSHIQRETSCSRPKLNSNWDADLYGYKWARDNVGOSGATIYRLY
/translation="MSHIQRETSCSRPKLNSNWDADLYGYKWARDNVGOSGATIYRLY
KREDAPELETKHGKGSVANDVTDEMYRLNMLTEFMPLPTIKHFIRTPDDAWLLTTAIP
GKTAROVLEEYPDSGENIVDDLAAVFLARLHSIPVCNCPFNSDRVFRLAQAGSMNNNGL
VDASDFDDERNGWPVEQVWKEMHKLLPFSPDSVVTHGDFSLDNLIFDEGKLIGCIDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYNPBEN66 3306 bp DNA circular SYN 06-FEB-1999 Cloning vector pBEN66 DNA for aminoglycoside 3'-phosphotransferase, beta-lactamase, complete cds.
                                     KpnI-DraII-Apal-Xhol-Sall-ClaI-HindIII-ECORV-ECORI-P9tI-Smal-BamHI-Spel-Xbal-NotI-XmalII-BstXI-SacII-SacI SELECTION #resistance Ap #indicator beta-galactosidase SUMMARY BluckSp #length 2964 #checksum 690.
                                                                                                                                                                                                                                                                                                                                                                                                                          /note="derived from Tn903; kanamycin resistance gene"
/citation=[2]
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D85525
D85521 GI:1345433
D85525
plasmid; aminoglycoside 3'-phosphotransferase; beta-lactamase.
Cloning vector pBEN66 (lab_host:E.coli) plasmid:pBEN66 DNA.
Cloning vector pBEN66
artificial sequence; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (23-MAY-1996) to the DDBJ/EMBL/GenBank databases.
Yoshihiro Yamamoto, Hyogo College of Medicine, Department of
Genetics: Mukogawa-cho 1-1, Nishinomiya, Hyogo 663, Japan
(Tel:0798-45-6587, Fax:0798-40-7639)
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"aminoglycoside 3'-phosphotransferase'/protein_id="BAA12824.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Y. and Furuyama, J.
One-step disruption by circular DNA in Escherichia coli
Unpublished (1996)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 DB 14; Length 2964;
                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Cloning vector pBEN66"
/plasmid="PBEN66"
/db_xref="texon:47800"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                               Score 70; DB 14; Le
Pred. No. 8e-12;
0; Mismatches 10;
1976-2764 789-1 (c) Ap-R; b-lactamase
                                                                                                                                                                                       construct"
                                                                                                                                                                                                                                723
                                                                                                                                                               1. 2964
/organism="synthetic or
/db_xref="taxon:32630"
3 736 c 755 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            746 GGGGGCCCGGTACCCAGCTTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="T3 promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                 47.0%;
88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ′gene≖"kan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="kan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260. .1075
                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 88.4
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamotc, Y
                     POLYLINKER
                                                                                                                                                                                                                                750 a
                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNPBEN66/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lacZ region is on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                             Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Currator Program.
BlueScribe KS Plus - Cloning vector
ENTRY BLUEKSP
TITLE BlueScribe KS Plus - Cloning vector
PATE 28-JAN-1987
#sequence 02-FEB-1987
#sequence 04-MAR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Stratagene
Polylinker region revised 03-APR-1987 according to Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to Stratagene COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
VecSource(3):bGalKS, GenBank(50):PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that the plus strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #journal Gene (1987) in press
#citation Sequence data from StrataGene
#comment sequence correction according to Stratagene COM
Obtained from StrataGene on floppy disc.
Revised 02-FEB-1987 by F. Pfelffer:
1409/10 'AT' to 'TA' to match revised sequence of PBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       start of T7-RNA synthesis (c) start of T3-RNA synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (c) BlueKS-polylinker (c) T3 promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T7 promoter
BlueKS-polylinker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conflict (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VecBase(3):BlueKSm, VecBase(3):BlueSKp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This vector contains the fl origin so the can be obtained upon fl superinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T3 promoter
pUC19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
5943-5488 (c) phage f1
236- 400 pUC19c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5943-5488 (c) phage f1
449-285 (c) pucl9
1-20 T7 promot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         puci9c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Features of BlueKSp (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Features of BlueKSp (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>0</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Θ
                                                                                                                                             Obtained from VecBase 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448-2617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VecBase(3):BlueM13p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2686- 754
                                           Synthetic construct DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                  artificial sequence.
1 (bases 1 to 2964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108-
                                                                                                                                                                                                                                                                                                                                                                                                    artificial
  GI:310729
                                                             synthetic construct
                                                                                                                                                                                                                                                                                                                                                                              ACCESSION VB007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626- 645
653- 760
772- 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      795-2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1032-2964
Conflict (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       643
                                                                                                                                                                                                                                                                                                                                                                                                                                                fnumber 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      795-1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #parent
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARENT
                                                               ORGANISM
                                                                                                                          AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                        REFERENCE
  VERSION
KEYWORDS
```

ORIGIN

```
/codon_start=1
/transl_table=11
/transl_table=11
/product-rel-chloramphenicol acetyltransferase"
/protein_id="ApC3619.1"
/db_xref="G1:984909"
/translation="MEKKITGYTTYDISOWHRKEHFBAFQSVAQCTYNQTVQLDITAF
/translation="MEKKITGYTTYDISOWHRKEHFBAFQSVAQCTYVFHEQTETF
SSLWSEYHDDFRQFHAIYSQDVACYGEDLAYFPKGFIENMFFVSANPWVSFTSFBLUY
ANMDNFFAPVFTMGRYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQXCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
DRWEPELNEAIPNDERDTTWPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     artificial sequence; vectors.

1 (Dases 1 to 4267)

21korski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1920 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACGGTGGTCGTCGAG 1979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 AGIGGAICCCCCGGGCTGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ONA circular SYN 14-SEP-19
prs304 with TRP1 marker, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 4267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 14; Length 41
Pred. No. 8.3e-12;
0; Mismatches 10; Indels
                                                                                               complement(join(3704. .4144,1. .219))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Cloning vector pRS304"
/db_xref="taxon:31827"
0965 c 1092 g 1082 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 8.3e-12;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                    1092 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.4%; Pred. No. 8
Matches 76; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1980 GGGGGCCCGGTACCCAGCTTTGTT 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2785 GGGGGCCCGGTACCCAGCTTTTGTT 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                City, UT 84132, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                          b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                                                                                                       959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRS304 4267 bp D
Yeast integrative vector
sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning vector pRS304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.0%;
llarity 88.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 4267)
Stillman, D.J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         U03436.
U03436.1 GI:416305
                                                                                                                                                                                                                                                                                                                                                                                                       1009 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 76; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89276910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1128
                                                                                                                                                                                                                                                                                                                                                                                                          1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
PRS304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="ampidillin resistance"
/function="ampidillin resistance"
/product "beta-lactanase"
/product "beta-lactanase"
/product "8104908".
/db_xref="GI:984908".
/db_xref="GI:9
                                                                                                                                                                                                                                                                    /product="beta-lactamase"
/product="beta-lactamase"
/brotein_id="baA12825.1"
/db_xref="G1:134436"
/translation="M845436"
IELDLNSGKILESFRREERFPWASIPRVLLCGAVLSRIDAGOEDGERRIHYSONDLVE
SRYTERKHITDGMTVRELCSAAITMSDNTAANLLITIGGPRELIAFLHNMGDHYTRL
DRMEPELNBAIPNDTTHWADWATTLRKLLTGELITLASRQGLIDWMEADKYRAPL
IRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVITTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hengen, P.N.
Direct Submission
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      elements
              RVGIADRYODLAILMNCLGEFSPSLQKRLFQKYGIDNPDMNKLQFHLMLDEFF"
complement(2209. .3069)
/gene="amp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      отеда
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloning vector pBSL159.
Cloning vector pBSL159
artificial sequence; vectors.

1 (bases 1 to 414)
Alexeyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omegfor Escherichia coli vector construction and in vitro dene 160 (1), 63-67 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         XXU35131 4144 bp DNA circular SYN
Plasmid pBSL159 cloning vector, complete sequence.
U35131.1 GI:984907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                            /note="amipicillin resistance gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Cloning vector pBSL159"
/plasmid="pBSL159"
/db.xref="taxon:42704"
complement(1129, .1989)
/EC_number="3.5.2.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 70; DB 14; I
Pred. No. 8.1e-12;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           862
                                                                                                        complement(2209. .3069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .4144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 GGGGGCCTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        790 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGGCCCGGTACCCAGCTTTTGTT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.0%;
88.4%;
                                                                                                                                                                                            /citation=[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 4144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95354958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Simi
Matches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
XXU35131
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
```

VERSION

g

ò 유 ð

į

```
Cloning vector pRS303.
                                                                                                                                                                                                                                                 2 (bases 1 to 4373)
Stillman, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 4443)
Stillman, D.J.
                                                                GI:416307
                                                                                                                                                                                                                                                                                                                                   City, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U03435.1 GI:416304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 88.4 Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                 U03438
U03438.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
                                 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89276910
                                                                                                                                                                                                                                                                                                                                                                                                                      1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                 ACCESSION
                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MIEQDGLHAGSPAAWVERLFGYDWAQQTIGCSDAAVFRLSAQGR
PVLEWYTDLGSGALNELQDEARLSWLATTGYPCAAVLDVYPEAGRDWLLLGEVPGQDL
LSSHLAPAEKVSIMADDARRLHTUPPATCPFDHQAKHRIERARTRMEAGLVDQDDLDE
EHQGLAPAELFARLFARMPDGEDLVYTHGDACLPNINVENGRFSGFIDCGRLGVADRY
ODIALATRDIAELGEEWADRFLVYGIAAPDSQRIAFYRLLDEFF"
/CC_number="3:5.2.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY IELDLNSGKILESFRPERFPMSFRVLCGAVLSRIDAGGEOLGRRIHYSONDLVE SVOTEKHLTDGMYVRELCSAAITMSDNTAANLLITIGGPKELTAFLHNMGDHYRL DRWEPELNAAIDHNEDTHWYRLLDTGELLTASROQLIDWMEDVAGFL LRSALPAGWFLIABROGAGENGSRGIIAALGPDGKPSRIVVIYTIGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                (bases 1 to 4289)
Hengen, P. N.
Direct Submission
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
1. 4289
                                                                                                                                               cloning vector pBSL97.
cloning vector pBSL97
artificial sequence: vectors.
1 (bases 1 to 4289)
Alexyev,M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omega elements for Escherichia coli vector construction and in vitro Gene 160 (1), 63-67 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2014 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                               26-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 14; Length 4289;
Pred. No. 8.3e-12;
0; Mismatches 10; Indels C
                                                               XXU35136 4289 bp DNA circular SYN Plasmid pBSL97 cloning vector, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="neomycin phosphotransferase"
/protein_id="AAC53629.1"
/db_xref="GI:984924"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="ampicillin resistance"
/product="beta=lactamase"
/protein_id="AAC53630.1"
/db_xref="GI:984925"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Cloning vector pBSL97"
/pbsamid="pBSL97"
/db_xref="taxon:47709"
complement(804. .1598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2074 GGGGGCCCGGTACCCAGCTTTTGTT 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 GGGGGCCTAACTAACTATTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1111 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.0%;
88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIGASLIKHW"
1157 c
                                                                                                  U35136
U35136.1 GI:984923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 88.4 Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                DEFINITION
                                                                                                                                                                  ORGANISM
                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                   AUTHORS
TITLE
                                                                                                                                                                                                                                                                                  JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                 xx035136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     유
```

13

RESULT PRS306

```
Direct Submission Submission Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake City, T 84132, USA
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                      Cloning vector pRS306.
Cloning vector pRS306
artificial sequence; vectors.
1 (base 1 to 4373)
Sikorski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae
69276910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning vector pRS303
artificial sequence; vectors.
1 (Dases 1 to 4443)
Sikorski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2026 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AGIGGAICCCCCCGGGCIGCAGGAATICGAIAICAAGCITAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRS303 4443 bp DNA circular SYN 14-SEP-1995
Yeast integrative vector pRS303 with HIS3 marker, complete
PRS306 4373 bp DNA circular SYN 14-SEP-1995
Yeast integrative vector pRS306 with URA3 marker, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 4373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Cloning vector pRS306"
/db_xref="taxon:31829"
1 987 c 1106 g 1099 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Cloning vector pRS303"
/db_xref="taxon:31826"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47.0%; Score 70; DB 14;
88.4%; Pred. No. 8.3e-12;
tive 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2086 GGGGGCCCGGTACCCAGCTTTTGTT 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 1. 4373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1109 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1048 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
```

Search completed: May 29, 2000, 21:35:38 Job time: 36870 sec

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LERPPPRWSSNSPYSESYYARYLVKHSTTPNGIPDDOEVPTAEEKPDVGEMITSELVLI
ETIALIAICHIVGKIYAQLLAGTAFELPTFVCVLFVGVILSNGLSINGFYRVFERAVS
VLGNVSLSLFLAMALMGLKLWELASLALPMLAILVVQTIFMALYAIFVTWRMYGKNYD
AAVLAAGHCGFGLGATPTAIANMQAITERFGPSHMAFLVVPMVGAFFIDIVNALVIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLLVMONAIGIGMASLLGLDPLMGLLAGSITLSGGHGTGAAWSKLFIERYGFTNATEV
AMACATFGLVLGGLIGGPVARQLTLTKGNKSWVPGPPSRSTVSISLISNSCSPGDPLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03-APR-1998) Gal J., Institute for Biotechnology, Bay Zoltan Poundation for Applied Research, Szeged, Derkovits fasor 2., 6726, HUNGARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="WEHLDTLATLVAATLTLLLGRKLVHSVSFIKKYTIPEPVAGGLL
VALALLVLKKSMGWEVNFDMSLRDPLMLAFFATIGLNANIASLRAGGRVVGIFLIVVV
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2106 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2165
                                                                      49 AGTGGATCCCCGGGCTGCAGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A positive selection cloning system based on the gltS gene of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 4670)
Gal.J., Szekeres,S., Schnell,R., Pongor,S., Simoncsits,A. and
Kalman,M.
                                      Gaps
                                      ö
                                                                                                                                                                                                                                                  ASAJ5326 4670 bp DNA circular SYN 08-FEI
pGAII(+) KS positive selection cloning vector glts gene
AJ005326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47.0%; Score 70; DB 14; Length 4670; 88.4%; Pred. No. 8.4e-12; tive 0; Mismatches 10; Indels (
Location/Qualifiers
1. .4670
/organism="synthetic construct"/db_rref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anal. Biochem. 266 (2), 235-238 (1999)
99107575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="qlutamate permease"
                                                                                                                                                                                                                                                                                                                      AJ005326.1 GI:4028984
gltS gene; glutamate permease.
synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 4670)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1441 GGGGGCCCGGTACCCAGCTTTTGTT 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA06473
/db_xref="G1:4028985
                                                                                                                                                                    2166 GGGGGCCCGGTACCCAGCTTTGTT 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1231 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGCCTAACTAACTATTTGTT 134
                                                                                                                                              109 GGGGGCCTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352. .2231
/gene="gltS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852. .2231
/qene="qlts"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.48
Matches 76; Conservative
       Query Match
Best Local Similarity 88.49
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040 a
                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                   ASAJ5326/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                   g
                                                                                                                                                   ò
```

_		Section 1					e e Ma
<u>.</u>	÷**	*. *				<b>*</b>	
d.	`#.a. ·				•	and the second s	
5° .	y .					**	* 1
ja E							
		,					
No.							
7							
At.	K.	to the second second					
4.			and the g	4.5			
	<b>W</b>						
			- ≽ ₁ ' '	*	* **	•	
a a							
19		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1					
						*	
		# ** *** *****************************		1 A T			
			en e	· · · · · · · · · · · · · · · · · · ·	***		
r Ma							
		· ·					2
		2 ⁹⁶ 8		計算を一支が 1		*	
**		•					
<b>1</b>							1.7.
**							
į.							
				•		•	
**************************************		š		× .			
					•	18 1	
ľ			e e e e e e e e e e e e e e e e e e e				
	•	*	4				
					e to pro-		
*							
					· 		**
					. T.		
F							
		•		en e		•	
<b>T</b>	9 (1)		46				
į.				· ·			
Total Control	A STATE OF THE STA				<i>y</i>		
p de							
						er de la companya de Na companya de la co	
<b>殿</b>				·			
10.00			£ 1				
*	· · · · · · · · · · · · · · · · · · ·	•					
				e e e e e e e e e e e e e e e e e e e			
							<u> </u>

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

May 29, 2000, 21:58:27 ; Search time 1446.77 Seconds (without alignments) 25.767 Million cell updates/sec Run on:

US-08-935-377-8

149 1 GGCCAAAAATTGAAAAACTA......TTGTTTTTGTGGGCCCGGCC 149 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

311585 segs, 125096042 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_36:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	azoospe	Nucleotide analogu	Polynucleotide seq		Human endogenous r	Human endogenous r	Plasmid pG+host4 c		Plasmid pG+host5 c	Plasmid pG+host6 c	Maize fluory2 gene	Swedish-FAD APP ta	London-FAD APP tar	Swedish/London-FAD	Swedish-FAD APP713	Human endogenous r	bDAT. cDNA encodin	DE19731274 Seq ID	Sed	PHAT	E. coll biotin DNA	Sed	DE19731274 Seq ID	Maize female-prefe	adogene	Stealth virus nucl	virus	-	544)	otide seq	lice. N	>	,
TANKING OF		ΙΩ	987664	T04866	X20513	V31294	T75006	T75005	048463	T39485	048464	048465	o	X24730	X24731	X24732	X24733	v68808	026664	X02815	X02813	T43794	X02800	X02814	X02812	V57377	T75010	V10190	V12003	T04575	V22271	V69740	4987	V64254	010
		90	-	-1	н		-	-	-	Н	н	-	-	<del>, -</del> 1	<b>~</b>	н	-	ч	П	-	П	П	-	-	Н	7	7	-	н	-	ч	~	ч	1	,
		Length	259	501	651	752	1001	1122	3792	4226	5234	6722	10529	12814	15692	15692	15701	545	2640	3481	3810	5356	84	3465	3794	6596	545	685	685	4164	4164	4164	5178	2973	2100
æ		Match						٠			٠	٠	٠	•		•	Š.	S.	'n	•	٠	•	٠	٠	•	٠	٠	٠	ä	40.3		ö	٠	σ.	o
		Score	71	70	89	89	89	68	68	69	89	68	68	68	68	68	89	7	^	66.2	ø	2	9	65	65		4	63.4	3	9	9	9		58.8	0
	Result	Q		7	m			φ υ		ω		c 10	_	12	13	14	15	-	_	c 18	-	~	21	~	c 23	24	c 25	<b>5</b> 6	27	28	53	30	31	32	cc

Candida CaRhol gen Clone #4 from muta Nucleotida sequenc E. coll biotin DNA Yeast RAD17 coding Plasmid pPK13/14 D Plasmid pPK5/6 DNA Plasmid pPK9/10 DN Plasmid pPK9/10 DN Plasmid pPK9/10 DN Vector pHP-1 compr Vector pHP-1
T92869 V57250 X05602 X05602 T91037 V64258 V64258 V64255 V64257 V64257 V64257 V64257
анаанаана
3198 459 1949 2150 2150 3956 4088 4102 4583 12494 10504
νουροροροροσιο
$\begin{array}{cccccccccccccccccccccccccccccccccccc$
ი ი ი ი ი ი ი ი ი ი ი ი ი ი ი ი ი ი ი
888888444444 489688644444
υυυ

## ALIGNMENTS

ö Chandley AC, Cooke HJ, Hargreave TB, Kun M, Sharkey AM;
WPI: 95-17021/22.
WRITHING A mode gequence and encoded polypeptide - may be used in the clinical diagnosis of male infertility.
Disclosure: Fig 5: 40pp; English.
A mouse gene partial sequence (087664) showing homology to the human azoospermia factor (AZF) YRMM gene was obtd. from mouse genomic phage clone M3.2 isolated from a genomic library screened with MYK (YRRMI) clone M3.2 isolated from a genomic library screened with MYK (YRRMI) of the mouse Y-chromosome. A full cDNA sequence (Q87665) was also obtd. 43 GCCATGAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGAC 102 Gaps /*tag= a
/note= "base n at position 174 is not identified
in the specification"
misc_difference 197 /*tag- b /note- "base n at position 197 is not identified in the specification" ó; Length 259; Indels 06-MAR-1996 (first entry) Mouse azoospermia factor (AZF) gene partial clone M3.2. Azoospermia factor: AZF; male infertility; YRRM gene; Y-chromosome; RNA recognition motif; ds. 69 T; Score 71.2; DB 1; Pred. No. 7.3e-16; 0; Mismatches 13; 63 G; 103 CTCGAGGGGGGCCTAACTAACTATTTGTT 134 27.4kr.1952. 24.OCT-1994; G92344. 22.OCT-1993; GB-021857. 07.JUL-1994; GB-013760. (MEDI-) MEDICAL RES COUNCIL. Chandley AC, COOKE HJ, Hargreave TB, 58 C; Key Location/Qualifiers misc_difference 174 Q87664/c ID Q87664 standard; DNA; 259 BP. AC Q87664; 47.8%; ilarity 85.9%; Conservative 67 A; Query Match Best Local Similarity Matches 79; Conserv Seguence 259 BP; Mus sp. g ò ద å

59

T04866 standard; DNA; 501 BP. T04866; 7 RESULT TO4866

Ĥ

149

152 G;

167 C;

180 A;

```
651 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence
                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                 요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reeve MA, Robbison PS;

Prever MA, Robbison PS;

PT Reeve MA, Robbison PS;

PT Reeve MA, Robbison PS;

PT Reeve MA, Robbison PS;

PT Pass 20290/42

PT Pass calling of residual fluorescence labelled nucleotide analogues - to prevent migration in electrophoretic sequencing gel and interference with base calling of DNA chains PS Example; Fig 1; 18pp; English.

Example, Fig 1; 18pp; English.

Example Fig 1; 18pp; English.

C The invention concerns the modification in electrophoretic labelled nt analogues to prevent migration in electrophoretic concerns the modification in or prevent with base calling of DNA chains. The modification involves the use of a phosphatase enzyme to remove at modification involves the use of a phosphatase enzyme to remove at cleast one 5'-phosphate pp. The nts were prepared using ABI Amplitted dye-terminating kt. The template used was I microg. of MI3 mp8. The primer was MI3 Universal primer. Samples were recovered. Some were primer was MI3 Universal primer. Samples were digestion. This collines TO4865, TO4867 was a control nt. which was not treated with includes TO4866. TO4887 was a control nt. which was not treated with calkaline phosphatase. The example shows that alkaline phosphatase.

C treatment causes removal of the dye-terminator artefacts and allows for accurate base calling with the ABI analysis software.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Figure 1. Cm; wp1; 99-081273/07.

New isolated Treponema pallidum nucleic acids - used to develop new isolated Treponema pallidum nucleic scharacterisation, prevention products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis Claim 1; Page 257; 1150pp; English.

X00500-21243 represent polynuclectide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1996 (first entry)
Nucleotide analogue treated with calf intestinal alkaline phosphatase.
Nucleotide analogue; alkaline phosphatase; ss.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AGIGGAICCCCCGGGCCIGCAGGAATICGAIAICAAGCTIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequence from the genome of Treponema pallidum. Treponema pallidum infection; syphills; Borrella infection; animal; enzyme production; ds. Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.0%; Score 70; DB 1; Length 501; 88.4%; Pred. No. 2.4e-15; tive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                           1. .501
/*tag= a
/note= "std. IUPAC codes used"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GGGGGCCTAACTAACTATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 GGGGGCCCGGTACCCAGCTTTTGTT 141
                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-DEC-1998.
23-JUN-1998.
24-JUN-1997: US-050667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X20513 standard; DNA; 651 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X20513;
05-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                WO9524505-A.
14-SEP-1995.
07-MAR-1995; G00490.
08-MAR-1994; EP-301636.
(AMSH ) AMERSHAM INT FLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.4
Matches 76; Conservative
                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X20513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DATO DE LA PERENTA DE LA PEREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                       ð
```

```
PD 28-MAY-1998.

21-NOV-1997; US-061953.

PR 14-OCT-1997; US-061953.

PR 22-NOV-1996; US-031626.

PA (HUMA-) HUMAN GENOME SCI INC.

PA (HUMA-) HUMAN GENOME SCI INC.

Choi GH, Dillon PJ, Welch RA;

WPI: 98 312461/27.

New isolated uropathogenic E. coli nucleotide sequences - used to avealop products for the detection of pathogenic E. coli and to relate nimmune response to pathogenic E. coli and to presents a pathogenic E. coli and to claim 21; Page 221-222; 250pp; English.

Claim 21; Page 221-222; 250pp; English.

Craim 21; Page 221; Pag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AGIGGAICCCCGGGGTGCAGGAAITCGAIAICAAGCITAICGAIACCGIGGACCTGGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 14
                                                                                                                                          49 AGIGGAICÉCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT: 5
T75006/c
L75006 standard; DNA; 1091 BP.
AC T75006 standard; List entry)
DT 06-0CT-1997 (first entry)
DE Human endogenous retroviral sequence 6.
KW Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine; ss.
                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 G;
   45.6%; Score 68; DB 1; L4
100.0%; Pred. No. 1.3e-14;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45.6%; Score 68; DB 1; 3 100.0%; Pred. No. 1.4e-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Pred. No. 1.4 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          162 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                v31294/c
ID v31294 standard; DNA; 752 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 68; Conservative
               Query Match
Best Local Similarity 100.0
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              752 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                        109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                          137 GGGGGGCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 GGGGGCC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09822575-A2.
```

```
This of this and the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-1994 (first entry)
Plasmid pG+host4 containing Ts replication system.
Temperature sensitive replication; antibiotic resistance marker gene site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human steroidogenesis acute regulatory protein genomic DNA. Human; steroidogenesis; acute regulatory protein; hStAR; analysis; mutation; detection; prenatal; genetic defect; congenital; protein; lipoid adrenal hyperplasis; treatment; prevention; gene; replacement therapy; hypercholesterolaemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated human steroidogenesis acute regulatory protein gene - used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           742 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%; Score 68; DB 1; Le
100.0%; Pred. No. 2.3e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           552 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-SEP-1993.
12-MAR-1993; F00248.
13-MAR-1992; F3-003034.
(INRG ) INRA INST_NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), Miller WL, Strauss JF;
96-443130/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   maintained at 28 deg.C.
Sequence 3792 BP; 1249 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T39485 standard; DNA; 4226 BP.
                                                                                                                                                                                                                               Q48463 standard; DNA; 3792 BP.
Q48463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
(UYPE-) UNIV PENNSYLVANIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-MAR-1996; UO3896.
23-MAR-1995; US-410540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3482 GGGGGGC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GGGGGGCC 116
109 GGGGGGCC 116
                                                                   49 GGGGGCC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
WO9629338-A1.
26-SEP-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9318164-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T39485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin D,
WPI; 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               œ
                                                                                                                                                                                       RESULT
Q48463/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T39485
                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ID DATE OF THE PARTY OF THE PAR
                                                                       ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   To the prognosis, diagnosis and monitoring of human cancers, especially breast cancer.

To the prognosis, diagnosis and monitoring of human cancers, respecially breast cancer.

Claim 10; Page 30-31; 74pp; English.

Claim 10; Page 30-31; 74pp; English.

Claim 10; Page 30-31; 74pp; English.

Cand 11-22 (T75003-10) were obtd. by screening human genomic libraries using human breast tumour-associated retroviral element libraries using human breast tumour-associated retroviral element.

B18Ag1 (see also T75002) as probe. These non-contiguous sequences in entrovirus genome (see also T75001). B18Ag1 and the other retrovirus sequences can be used in genetic vaccines and for the prognosis, diagnosis and monitoring of human breast cancer.

Sequence 1122 BP; 260 A; 316 C; 185 G; 279 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTGACCTCGAG 108
                                                                                                                                                                                                                                                       Endogenous human tumour-associated retroviral element, B18Ag1 - used for the prognosis, diagnosis and monitoring of human cancers, especially breast cancer claim 10; Page 31-32; 74pp; English.

Human endogenous retroviral sequences 10, 11-29, 3, 6, 12, 13, 14 and 11-22 (775003-10) were obtd. by screening human genomic libraries using human breast tumour-associated retroviral element B18Ag1 (see also 775002) as probe. These non-contiguous sequences lie in order 11-22, 14, B18Ag-1, 13, 12, 10, 3, 11-29, 6 in the retrovirus genome (see also 775001). B18Ag1 and the other retrovirus sequences can be used in genetic vaccines and for the prognosis, diagnosis and monitoring of human breast cancer. Sequence 1091 BP; 79 A; 350 C; 97 G; 248 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human endogenous retrovital sequence 3.
Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine;
Human retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 45.6%; Score 68; DB 1; Length 1091; 1 Similarity 100.0%; Pred. No. 1.5e-14; 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 68; DB 1; I
Pred. No. 1.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.6%; Scott No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
T75005/c
ID T75005 standard; DNA; 1122 BP.
AC T75005;
AC T75005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-1997, U00398.
10-JAN-1997, U0-587329.
(CORI-) CORIXA CORP.
Frudakis IN, Smith JM;
WPI: 97-384982/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Conservative
                       17-JUL-1997;
10-JAN-1997; U00398.
10-JAN-1995; US-587329.
(CORI-) CORIXA CORP.
Frudakis TN. Smith JM;
WPI; 97-384982/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 GGGGGCC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9725431-A1.
```

Matches

õ

DEPARTMENT OF STREET OF ST

Matches

셤

ð

g

ç

ö

ö

Indels

1249 T;

ö

```
6412 GGGGGGC 6405
                                                                                                                     5234 BP;
                                                                                                                                                                                                                                                                                                             4924 GGGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGGCC 116
                                                                                                                                                                                                                                                                                109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9318164-A.
                                                                                                       bacteria.
                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                  048465;
                                                                                                                                                                                                                                                                                                                                                         ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                 δ
      88888888888
                                                                                                                                                                                                                                                                                                                ô
for detection of mutation(s) of this gene that cause congenital

Ilpoid adrenal hyperplasia

Claim 1: Pages 23-25: 89pp; English.

Crap present sequence encodes the human steroidogenesis acute

regulatory protein (hStAR). The hStAR gene can be analysed for

mutations to detect (e.g. prenatally) genetic defects associated

Crap congenital 11poid adrenally hyperplasia (CAH), or its

transmission to children. CAH can be treated by protein or gene

Craplacement therapy, which can also be used to prevent or treat

Nepercholesterolaemia.

A human adrenal cortex CDNA library was screened with a mouse StAR

Creplace protein. When it was cloned into pSpoRT and expressed in

COS-1 cells cotransfected with pP450scc abd pADX, it increased the

Creation of pregnenolone synthesis from cholesterol or

Consultation of pregnenolone synthesis from cholesterol or
                                                                                                                                                                                                                                                                                                                                                                       4148 AGTEGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 4207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           remperature sensitive replication; antibiotic resistance marker gene; site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New bacterial plasmid contg, heat sensitive replication system and marker gene, opt. capable of chromosomal integration, used to inactivate specific gene or introduce heterologous gene brample 2; Fig 10; 73pp; French.

Example 2; Fig 10; 73pp; French.

Plasmid pGKL2 (Appl. BDviron. Microbiol., 48; 726 (1984)) contg. two antiblotic resistance marker genes was subjected to mutagenesis with hydroxylamine. A heat-stable mutent was isolated (coding for a heat-sensitive RepA - see Q48466 and Q48467), cut with ClaI and HpaII and sensitive RepA - see Q4860 and Q48467), cut with ClaI and HpaII and 445bp PvuII fragment lacking the Cm resistance gene was ligated to a 445bp PvuII fragment of pBluescript SK+ containing a multicloning
                                                                                                                                                                                                                                                                                                                                           49 AGIGGAICCCCCGGGCIGCAGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                           Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "origin of replication from pBR322"
2640. 4383
/*tag= b
/note= "from pGK12 (derived from pWV01)"
4384. 4786
/*tag= c
/note= "from pUB110"
                                                                                                                                                                                                                                                                                   Length 4226;
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                            1144 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-WAR-1994 (first entry)
Plasmid pG+host5 containing Ts replication system.
                                                                                                                                                                                                                                                                                                   .4e-14;
                                                                                                                                                                                                                                                                                      DB 1;
2.4e-1
                                                                                                                                                                                                                                                                                45.6%; Score v., 100.0%; Pred. No. 2.4e
                                                                                                                                                                                                                                            1132 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1993.
12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG ) INRA INTENAT RECH AGRONOMIQUE.
Gruss A, Maguin E;
WPI; 93-303478/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
36. .1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= ORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "from pSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74/c
Q48464 standard; DNA; 5234 BP.
Q48464;
18-MAR-1994 (first entry)
                                                                                                                                                                                                                                              940 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= //not
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     4208 GGGGGGCC 4215
                                                                                                                                                                                                                                                                                                                                                                                                        109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9318164-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                     a
```

```
New bacterial plasmid contg. heat sensitive replication system -
mearker gene opt. capable of chromosomal integration, used to
and marker gene opt. capable of chromosomal integration, used to
an inactivate specific gene or introduce heterologous gene
Disclosure; Fig 11; 73pp; French.

Disclosure; Fig 11; 73pp; French.

Plasmid pGK12 (Appl.Environ.Microbiol., 48; 726 (1984)) contg. two
antiblotic resistance marker genes was subjected to mutagenesis with
dydroxylamine. A heat-stable mutant was isolated (coding for a heat-
sensitive RepA - see Q48466 and Q48467), cut with Clal and Hparl and
sensitive RepA - see Q48466 and Q48467), cut with Clal and Hparl and
the 3340bp fragment lacking the Cm resistance gene was ligated to a
445bp Pvull fragment of pBluescript St+ containing a multicloning
site, T7 and T3 promoters and sequencing primer binding sites. The
resulting plasmid was designated pVE604 (or p6+host4 - Q8463).

To facilitate cloning in E.coll, the Ava-'EcoRI fragment of pBR322
containing the origin of replication and the ampicillin resistance
peh-host6 (Q48466). The pBR322 ORI allows maintenance of the plasmid in
E.coll at 37 deg.C. while the heat-sensitive ORI allows maintenance
of the pram-positive bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4984 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 4925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 49 AGTGGATCCCCCGGGCCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid pG+host6 containing Is replication system.
Temperature sensitive replication; antibiotic resistance marker gene; site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
site, T7 and T3 promoters and sequencing primer binding sites. The resulting plasmid was designated pVE6004 (or pG+host4 - Q48463). To facilitate cloning in E.coli, the 1.4kb AvaI-AlwNI fragment of pBR322 (containing the origin of replication) was inserted into NsiI-cleaved pG+host4 to give pG+host5 (Q48464).The pBR322 ORI allows maintenance of the plasmid in E.coli at 37 deg.C. while the heat-sensitive ORI allows maintenance at 28 deg.C in gram-positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1980 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                          1559 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 6722;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 5234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1503 G;
                                                                                                                                                                                                                                                                                                              1133 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              45.6%; Score 68; DB 1; Le 100.0%; Pred. No. 2.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1278 C;
                                                                                                                                                                                                                                                                                                                  973 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1993.
12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG ) INRA INST NAT RECH AGRONOMIQUE.
Gruss A, Maguin E;
WPI; 93-303478/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1961 A;
                                                                                                                                                                                                                                                                                                                  1569 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q48465 standard; DNA; 6722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 68; Conservative
```

```
Conservative
                                                                                                                                                                                                                                         25-FEB-1999.
18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                  (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9947 GGGGGCC 9954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GGGGGCC 116
                                                                                 sapiens.
                                                                                                                           mat_peptide
                                                                                                                                                                                   mat_peptide
                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                 Wirak DO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŘESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X24731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŏ
KEEKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Fig 1A-H; 37pp; English.

This is the nucleotide sequence of a clone of the fluory2 (fl2)

This is the nucleotide sequence of a clone of the fluory2 (fl2)

gene of maize. It codes for a 24-kDa alpha-zein protein (see W2397) that includes a 21-maino acid signal peptide (see W23976)

which targets the alpha-zein to the lumen of the rough endoplasmic reticulum. A claimed cereal plant contains a transgene comprising a first polynucleotide that encodes the fl2 signal peptide and a second polynucleotide that encodes an agronomically high-value treaff, and a transgene that also includes the fl2 promoter. The second polynucleotide preferably encodes a protein that has a high contained of Met, Lys, Try and/or Thr so that feeds from transformed maize, wheat, rice, barley, millet or sorghum will have increased contents of these essential amino acids in their seeds (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cereal plants containing trans-gene expressing fusion that includes signal peptide of the fl2 maize gene - and protein having high content of essential amino acids, producing feeds of improved nutritional value
                                                                              20-JUL-1998 (first entry)
Malze fluory2 gene (fl2).
Floury2, fl2 gene: alpha-zein; signal peptide; transgenic plant; seed; essential amino acid; animal feed; malze; rice; wheat; barley; millet; sorghum; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 10529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2262 G;
                                                                                                                                                                                            /*tag= a /note= "vector-derived sequence" /61. 3824 /*tag= "Claim 14" 3825. 4613 /*tag= c 3825. 3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.6%; Score 68; DB 1; Le
100.0%; Pred. No. 3.3e-14;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2484 C;
                                                                                                                                                                   Location/Qualifiers
1...760
                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1996; US-021833.
(PION-) PIONEER HI-BRED INT INC.
(UTAR-) UNIV ARIZONA STATE.
BEGCH L, COLEMBN CE, LAIKINS BA;
WPI: 98-110609/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2845 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X24730 standard; DNA; 12814 BP. X24730;
                                                     V09028 standard; DNA; 10529 BP
                                                                                                                                                                                                                                                                              68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10529 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGGCC 660
                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                             mat_pept1de
                                                                                                                                                        Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
X24730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
```

CDS

DAG XXXX DAG XXX DAG

```
T disease

Example: Page 95-103; 209pp; English.

Example: Page 95-103; 209pp; English.

This is the nucleotide sequence of Swedish-FAD APP targetting

control of the facilitates the introduction of one or more specific

strategy that facilitates the introduction of one or more specific

mutations into any gene in a single double reciprocal homologous

contentions into any gene in a single double reciprocal homologous

recombination step. The method has been used particularly for

introducing a humanised amyloid precursor protein (APP) gene into

condents for producing animal models of Alzheimer's disease (AD).

Condents for producing animal models of Alzheimer's disease (AD).

Condents for producing animal models of Alzheimer's disease (AD).

Condents for producing animal models of Alzheimer's disease (AD).

Condents for producing animal models of Alzheimer's disease (AD).

Condents for producing animal models of Alzheimer targetting

condents applied to embryonic stem cells. In each line, the mouse

condents applied to encode a mouse/human hybrid (m/hAPP) where

condents diseased of APP gene was modified to encode a mouse/human cDNA

condents for producing animal expand of APP770 were encoded by human cDNA

condents for producing animal expand of APP770 were encoded by human cDNA

condents for producing animal encoded a mouse (exons 16-18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 99-181029/15.
P-PSDB; W97997, W97998.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 amino acid differences exist between the mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The exon-cDNA fusion gene therefore encodes an APP containing a humanised beta-amyloid domain. In line ES5007, created using vector pMTI-2398, the Swedish mutation. i.e. KM(670,681)NL, was also introduced. The targetted Swedish-FAD m/hAPP gene expressed m/hAPP protein at levels approaching those observed for mouse APP in brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
21-JUN-1999 (first entry)
Swedish-FAD APF targetting vector pMTI-2398.
Amyloid precursor protein; APP; human; gene targetting;
homologous reccmbination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pMTI-2398;
Swedish-FAD APP; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45.6%; Score 68; DB 1; Length 12814; 100.0%; Pred. No. 3.5e-14; Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X24731;
21-JUN-1999 (first entry)
London-FAD APP targetting vector pMTI-2453.
Amyloid precursor protein; APP; human; gene targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /standard_name= Swedish-FAD APP
/note= "encodes W97997"
5369. .6160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
/note= "encodes W97998"
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1932. .2276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X24731 standard; DNA; 15692 BP.
```

ö

윱 à

ç

```
Example; Page 14-12.3 'UVPPP; ENGISEA, CONDON-FAD APP targetting vector pwr1-2454. The invention provides a novel gene targetting vector pwr1-2454. The invention provides a novel gene targetting vector pwr1-2454. The invention provides a novel gene targetting vector pwr1-2454. The invention provides a novel gene targetting vector protein a single double reciprocal homologous recombination step. The method has been used particularly for introducing a humanised amyloid precursor protein (APP) gene into introducing animal models of Alzheimer's disease (AD). Independent lines of transgenic mice (lines ES5007, ES5103, and ES5403) have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse technique applied to embryonic stem cells. In each line, the mouse applied to encode a mouse/human hybrid (m/hAPP) where sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 amino acid differences exist between the conse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The exon-cDNA fusion gene therefore encodes an APP containing a humanised beta-amyloid domain. In line ES5103, created using vector phr1-2454, the London mutation. In line ES5103, introduced. The targetted Swedish/London ThatPP gene expressed introduced. The targetted Swedish/London FAND m/hAPP gene expressed introduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W97998, W98000.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999 (first entry)
Swedish-FAD APP713 targetting vector pMTI-2454.
Amyloid precursor protein; APP; human; gene targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.6%; Score 68; DB 1; L 100.0%; Pred. No. 3.7e-14;
London-FAD APP; Swedish-FAD APP; mutation; ss.
Homo sapiens.
                                                                                                                                                                                                                                         /standard_name= "Swed1sh-FAD"
                                                                                                                                                                                                                                                                       replace(4989,"")
/standard_name= "London-FAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2731 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
45.6%; Score 68; DB
Best Local Similarity 100.0%; Pred. No. 3.7
Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      /note= "encodes W97998"
                                                                                                                                                                /note= "encodes W98000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Page 114-123; 209pp; English.
                                                                                 Location/Qualiflers 4807. .5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2423 A;
                                                                                                                                                                                        replace(4849,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X24733 standard; DNA; 15701 BP. X24733;
                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1997; WO-U14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15692 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12825 GGGGGGCC 12832
                                                                                                                                                                                                                                                                                                                                                                                                                            25-FEB-1999.
18-AUG-1997; U14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER CORP. Wirak DO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 99-181029/15
                                                                                                                                                                                                                                                                                                                                                                                                       WO9909150-A1
                                                                                                                                                                                                                                                                                                                          mat_peptide
                                                                                                            mat_peptide
                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in brain
                                                                                                                                                                                                mutation
                                                                                                                                                                                                                                                                            mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X24733
ID X24
AC X24
AC X24
DT 21-
DE SWE
KW AMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example; Page 104-113; 209pp; English.

Example; Page 104-113; 209pp; English.

This is the nucleotide sequence of London-FAD APP targetting
rector pMT-2453. The invention provides a novel gene targetting
strategy that facilitates the introduction of one or more specific
mutations into any gene in a single double reciprocal homologous
certor population step. The method has been used particularly for
introducing a humanised amyloid precursor protein (APP) gene into
codents for producing animal models of Alzheimer's disease (AD).

Introducing a humanised amyloid precursor protein (APP) gene into
codents for producing animal models of Alzheimer's disease (AD).

Essagina Essagin and Essagin transgenic mice (lines Esso).

Essagina Essagin to embryonic stem cells. In each line, the mouse
technique applied to encode a mouse/human hybrid (m/hAPP) where
amino acid residues 666-770 of APP/70 were encoded by human cDNA
sequences instead of mouse genomic exons (exons 16-18). Within
these residues, only 3 amino acid differences exist between the
mouse and human proteins, i.e. Gly-676 to ARG, Phe-681 to Thr and
Arg-684 to His. The exon-ONA fusion gene therefore encodes an APP
containing a humanised beta-amyloid domain. In line ESS401,
created using vector pMTI-2453, the London mutation. i.e.

V(7/17)L, was also introduced.
Sequence 15692 BP; 2423 A; 2730 C; 2786 G; 2541 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DD 12765 AGTGGATCCCCCGGGGTGCAGGAATTCGATATCAAGCTTATCGATATCGATACGTCGACGAGAG 12824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AGIGGAICCCCCGGGCTGCAGGAAITCGAIAICAAGCITAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W97998, W979999.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised anyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-1999 (first entry)
Swedish/London-FAD APP targetting vector pWII-2454.
Amyloid precursor protein; APP; human; gene targetting;
homologous recombination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pWII-2454;
        homologous recombination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pMTI-2453;
London-FAD APP; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 15692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.6%; Score 68; DB 1; L. 100.0%; Pred. No. 3.7e-14; tive 0; Mismatches 0;
                                                                                                                                                                                                        /*tag= a /*tag= "Swedish-FAD" /standard_name= "Swedish-FAD" /note= "encodes W97999" replace(4990,"")
                                                                                                                                                                                                                                                                                                                                   /standard_name= "London-FAD"
8223. .9023
                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/note= "encodes W97998"
                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X24732 standard; DNA; 15692 BP. X24732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 12825 GGGGGGCC 12832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999.
18-AUG-1997; U14507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 99-181029/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9909150-A1.
                                                                                                            Homo sapiens
                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                          mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
X24732
```

ö

Gaps

; 0

KWKE

ò

á

Length 15692; 0; Indels

2542 T;

2783 G;

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example: Page 124-133; 209pp; English.

Example: Page 124-133; 209pp; English.

This is the nucleotide sequence of Swedish-FAD APP713 targetting vector puri-255. The invention provides a novel gene targetting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous compliantion step. The method has been used particularly for introducing a humanised amyloid precursor protein (APP) gene into rodents for producing animal models of Alzheimer's disease (AD).

Introducing a humanised amyloid precursor protein (APP) gene into rodents for producing animal models of Alzheimer's disease (AD).

English and ES5401 and ES5403 have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse technique applied to embryonic stem cells. In each line, the mouse amino acid residues (66.770 of APP770 were encoded by human cDNA sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 amino acid differences exist between the containing a humanised beta-amyloid domain. In line ES5215, containing a humanised beta-amyloid domain. In line ES5215, Expected and also a stop codon (7 to Stop at position 714).

Sequence 15701 BP; 2470 A; 2675 C; 2845 G; 2497 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD 12774 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGACCTCGAG 12833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPT: 99-181029/15.
WPT: 99-181029/15.
WPPSDB; W97998, W98001.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protectin gene into rodents for producing models of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pWTI-2455; Swedish-FAD APP713; mutation; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.6%; Score 68; DB 1; Length 15701; 100.0%; Pred. No. 3.7e-14; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "Swedish-FAD"
replace(4981,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= APP713stop
8232. .9032
/*tag= d
                                                                                                                                                                                                                                                            /*tag= a
/note= "encodes W98001"
replace(4835,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "encodes W97998"
                                                                                                                                                                              Location/Qualifiers
4807. .4983
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999.
18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 68; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 12834 GGGGGGCC 12841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09909150-A1.
                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mat_peptide
                                                                                                                                                                                                                                                                                                                           mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
       NAMES OF THE PROPERTY OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
```

Search completed: May 29, 2000, 21:58:33 Job time: 38181 sec

•		\$	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	graph was an man garage.					e e
			•				\$	• • •	1
					4 **				1
								*	
	12, 1								
									1
		e.							
									ż
								-	* *
•			*						
					*			*	
	4				A				
					et et e				
				·			•	-	
				•			***		
						is the			
	į,							•	
				•					
			A		<i>.</i>				2 ·
•	*.								
			,	A STATE OF THE STA		e Page			
*				\$\$5	•			٠.	
			29. juli		g de la company				******
n .					en e				
						Ĭ.	N .		,
	4			1					
								1 2	
			- 198 - 198	1 . The state of t		N. C.		.t.	ā
×	at .		A. Santa						
A. A.				er griff					
	-								
ء الله عن			A paylong	ing the second of the second o					
	•								
	os Light of the co								
	7; <b>5</b> /			$\frac{\mathbf{x}_{i}}{\mathbf{x}_{i}} = \frac{\mathbf{x}_{i}}{\mathbf{x}_{i}} = \mathbf{$					
				\$ - x	•				1
		±1.00 mg/s							,
r .		en e				4			
								Mage All Francisco	
	je							7 7 44	
								All Control	
			•	•	•			and Arman Salahan Salahan Salahan	
1000			A	•	٧,				
				1 1			•	a sur	Ž
								- 1 <b>4</b>	•
				1.4			*		¢
				4 1					
•							· ·		

```
TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                             RESULT 1
US-08-992-334-1/C
47.6
47.6
47.6
47.4
47
 72778888888888888444444
78668888888888444444
                                                           00000
                                                                                             May 29, 2000, 22:09:05; Search time 621.83 Seconds (without alignments) 31.146 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appli
Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                        149
1 GGCCAAAAATTGAAAAACTA.......TTGTTTTTTGTGGGCCGGGC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednence sed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             /cgnl_6/ptodata/1/ina/5A_COMB.seq:*
/cgnl_6/ptodata/1/ina/5B_COMB.seq:*
/cgnl_6/ptodata/1/ina/5C_COMB.seq:*
/cgnl_6/ptodata/1/ina/5D_COMB.seq:*
/cgnl_6/ptodata/1/ina/6_COMB.seq:*
/cgnl_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgnl_6/ptodata/1/ina/PCTUS_COMB.seq:*
              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08 410-540-3

US-08-992-334-2

US-08-992-334-3

US-08-992-334-3

US-08-952-541-121

US-08-957-541-121

US-08-453-115-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-465-388-56

US-08-444-115-15

US-08-194-46028-15

US-08-198-4468-1
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                           230463 segs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                       nucleic search, using sw model
                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_NA:*
                                                                                                                                                         US-08-935-377-8
                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                 Scoring table:
                                                                        OM nucleic
                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      υo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        000000
```

```
Sequence 3, Appli
Sequence 116, App
Sequence 116, App
Sequence 5, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
US-08-464-051-3
US-08-462-498-3
US-08-967-1116
US-08-793-610-5
US-08-793-610-5
US-08-793-610-5
US-08-870-719-8
US-08-897-719-8
US-08-325-071-62
US-08-325-071-62
US-08-343-733A-1
US-08-465-948A-3
US-08-465-948A-3
US-08-465-948B-35
US-08-465-388-35
US-08-465-388-35
                                                                                                                                                                                                    US-08-789-354-1
US-08-680-395-4
US-08-596-300A-5
```

## ALIGNMENTS

```
Sequence 1, Application US/08992334

Patent No. 5919678

GENERAL INFORMATION:
APPLICANT: Maguin, Emmanuelle
TILLE OF INVENTION: PLASMID
TITLE OF INVENTION: PLASMID
TITLE OF SEQUENCES: 3
CORRESPONDENCE 3
CORRESPONDENCE ADDRESS: CARESTEL PATER
STREET: 350 West Colorado Boulevard, Suite 500
                                                                                                                                                                                                                                                                                                                                                                               ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION NUMBER: PCT/FF83/00248
APPLICATION NUMBER: PCT/FF83/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION NUMBER: FF892/03034
FILING DATE: 13-MAR-1992
ATTORNEY, AGENT INFORMATION:
NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: C93:31779
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERS: C557-8800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERS: C557-8800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION UNMERS: US/08/992,334
FILING DATE: 17-DE-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                       STREET: 350 West Colorad
CITY: Pasadena
STATE: California
COUNIRY: United States
ZIP: 91105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGIH: 3792 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
```

```
APPLICANT: Strauss III, Jerome F.

IIILE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto
CITY: Palo Alto
STREET: 6A
STREET: CA

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 2781..2782
OTHER INFORMATION: /note= "interruption of sequence data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1433..1434
OTHER INFORMATION: /note= "interruption of sequence data"
PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: -
LOCATION: 2208..2209
OTHER INFORMATION: /note= "interruption of sequence data"
                                                                                                                                                                                                                                                                       STATE: CA
COUNTRY: US
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,540
FILING DATE: 23-MR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: 30,092
REFERENCE/DOCKET NUMBER: 0CAL-238/00US
TELEPAATION NUMBER: 30,092
REFERENCE/COMMUNICATION INFORMATION:
TELEPAATION NUMBER: 30,093
TELEPAATION TO SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4016 base pairs
TYPE: NUCLEIC caid
STRANDBNESS: double
TYPE: TOUCLEIC caid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
3031..3765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
1620..1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
2567..2751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
2828..2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2956..2957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
2267..2425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
2047..2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 AGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3792;
                                                                                                                                                                                                                                  Length 3792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 6.6e-15;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 6.6e-15;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FF 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 FR/93/00248
TPILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/08410540
Patent No. 5807679
GENERAL INFORMATION:
APPLICANT: Miller, Walter L.
APPLICANT: Lin, Dong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-302-752-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                         HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL:
CLONE: pG+host4
US-08-992-334-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3482 GGGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-08-410-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
```

g ò 셤

ò

```
4984 AGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 4925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
         49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCS-08-992-334-3/c
Sequence 3, Application US/08992334
Sequence 3, Application US/08992334
Patent No. 591367
GENERAL INFORMATICN:
APPLICANT: Magulin, Emmanuelle
TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE
TITLE OF INVENTION: PLASMID
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS: Alexer & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                     Sequence 2, Application US/08302752

Sequence 2, Application US/08302752

Patent No. 6025190

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: THERMOSENSIBLE PLASMID

NUMBER OF SEQUENCES: 3

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER: DATE: Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,752

FILING DATE: 13-MAR-1992

PRIOR APPLICATION DATA:

FILING DATE: 13-MAR-1993

INFORMATION FOR SOQ ID NO: 2:

SEQUENCE CHARACTERIFICS:

LENGTH: 5234 base pairs

TYPE: nucleic acid

STRANDEDSS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 5234; 7.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.6%; brod. No. . . . . . 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-302-752-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Pasadena
STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                  4924 GGGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4924 GGGGGGCC 4517
                                                                                            109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GGGGGGCC 116
                                                                                                                                                                                                        RESULT 5
US-08-302-752-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                               ద
                                                                                            ö
                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                      3938 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 3997
                                                                                                                                                                                 49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08992334
Patent No. 5919678
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL INFORMATION:
CENERAL OF CHUSHODS
CHUSHODS
TITLE OF INVENTION:
CORRESPONDENCE 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                       ö
. OTHER INFORMATION: /note- "interruption of sequence data" US-08-410-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.6%; Score 68; DB 4; Length 5234; Best Local Similarity 100.0%; Pred. No. 7.4e-15; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                            Length 4016;
                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US/08/302,752
FILING BAPLICATION NUMBER: US/08/302,752
FILING BAPLICATION NUMBER: US/08/302,752
PRIOR APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR92/03034
FILING DATE: 13-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
STATE: California
COUNTRY: United States
21P: 91105
                                                                                       Ouery Match
Best Local Similarity 100.0%; Pred. No. 6.7e-15;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C93:31779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MADIOM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Prout, D. Bruce
REGISTRATION NUMBER: 20958
REFERENCE/DOCKET NUMBER: 203:
TELECOMMUNICATION INFORMATION:
TELEPAX: (626) 779-9900
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                               3998 GGGGGCC 4005
                                                                                                                                                                                                                                                                     109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                              US-08-992-334-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-992-334-2
```

```
ö
                                                                                                                                                                                                                                                                   48 GAGTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 107
                                                                                                                                                                                                                                         49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GGGGGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 61
                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.5%; Score 67.8; DB 3; Length 793; 86.2%; Pred. No. 4.5e-15; Live 0; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8

US-08-967-101-121/c
US-08-967-101
Sequence 121, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF SEQUENCES: 183
CORRESPONDENCE: ADDRESS:
                                                                                                                                                   Length 6722;
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/967,101 FILING DATE: 10-NOV-1997 CLASSIETCATION: 435 PRIOR APPLICATION DATE: APPLICATION DATE: APPLICATION DATE: APPLICATION NUMBER: 08/592,541
                                                                                                                                                   DB 5; Ler
8.1e-15;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                   Mismatches
                                                                                                                                                   Score 68;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
WEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_TOS
                                                                                                                                                   Query Match

Best Local Similarity 100.0%; P.
Matches 68; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic)
US-08-967-101-121
                                        TOPOLOGY: linear ; MOLECULE TYPE: DNA (genomic) US-08-302-752-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inear
                                                                                                                                                                                                                                                                                                                                                                  6412 GGGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                        109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         đ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.6%; Score 68; DB 4; Length 6722; Best Local Similarity 100.0%; Pred. No. 8.1e-15; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Date PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
UNRENT APPLICATION DATA:
                                                                                                                                                          CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION NUBER:
PRIOR APPLICATION NUBER:
FILING DATE: 24-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUBER: FR FF92/03034
FILING DATE: 13-MAR-1992
APPLICATION NUBER: 20958
REFERENCE/DOCKET NUBER: 20958
REFERENCE/DOCKET NUBER: 20959
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAM: (626) 52-9900
TELEFAX: (626) 577-8809
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO FR/93/00248
                                                                                                                  APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08302752 Patent No. 6025190 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
US-08-992-334-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGIH: 6722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111111
6412 GGGGGCC 6405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-302-752-3/c
```

g ò g

ò

윱

ŏ

```
50 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43.9%; Score 65.4; DB 3; Length 9318; 11arity 98.5%; Pred. No. 7.6e-14; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR.1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTONEY/AGENT INFORMATION:
ANDER APPLICATION NUMBER: DE 105 03 952.1
ATTONEX/AGENT INFORMATION:
ANDER APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 56, Application US/08463115
Patent No. 5703231
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSE: Lyon & Lyon STREET: 613 West Fifth Street STREET: Sulte 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A. ZIP: 90071-2066 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERNCE/DOCKET NUMBER: P1614-7007
TELECOMMUNICATION:
TELEPHONE: (202)638-5000
                                                             COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 9316 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: circular MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 66; Conserve
                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5714 GGGGGCC 5720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-463-115-56
                      CITY: Wa:
STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 GAGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 GGGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, CHIStopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERIAG, Wolfram
TITLE OF INVENTION: FOR GENE TRANSFER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: 183
CORRESPONDENCES: 183
CORRESPONDENCES: 183
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nikaido, Marmelstein, Murray & Oram LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 4;
4.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 67.8;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 GGGGGGCCTAACTAACTTTTGTT 134
108 GGGGGGCCTAACTAACTATTTGTT 134
                           60 GGGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 GGGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                                                                  US-08-592-541-121/c
: Sequence 121, Application US/08592541
; Patent No. 5986054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DALL.
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: PICCHEY, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
: TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-592-541-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-793-610-6
```

셤 ö

ò

```
49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Devine, Scott E.
APPLICANT: Devine, Jef D.
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
                                                                                                                                                                     Four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                           CLASSIFICATION: 4.0.5

PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below:
APPLICATION DATA: described below:
APPLICATION DATA: described below:
APPLICATION NUMBER: 00/157,811
FILING DATE: No. 5753488ember 23, 1993
APPLICATION NUMBER: 07/764,814
FILING DATE: May 22, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: May 22, 1991
APPLICATION NUMBER: 07/763,039
FILING DATE: May 23, 1991
APPLICATION NUMBER: 20, 1991
ATTORNEY AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 213/300
TELEFONETON TOWERER: 213/300
TELEFONETON TOWERER: 213/300
TELEFONETON: (213) 489-1600
TELEFONETON: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/204,675
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08204675; Patent No. 5677170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.1%;
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 100. CITY: Washington STATE: D.C. COUNTRY: U.S.A. 7TP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: US-08-465-388-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 GGGGGGNC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AGIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/157,811
FILING DATE: No. 570321ember 23, 1993
APPLICATION NUMBER: 07/704,814
FILING DATE: May 22, 1991
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/704,814
FILING DATE: September 20, 1991
APPLICATION NUMBER: 32,327
FILING DATE: September 20, 1991
APPLICATION NUMBER: 32,327
FILING DATE: September 20, 1991
APPLICATION NUMBER: 32,327
FILING DATE: NAPLON: NICORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELEFRAX: (213) 489-1600
TELEFRAX: (213) 489-1600
TELEFRAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 56, Application US/08465388
Patent No. 5753488
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES;
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES:
ADDRESSEE: Lyon & Lyon
STREET: SLIVE 4700
STREET: SLIVE 4700
CITY: Los Angeles
STATE: California
COUNTRY: US.A.
COMPUTENT SADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 94.1%; Pred. No. 1.5e-13;
Matches 64; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSeq Version 1.5 CURRENT APPLICATION DATA:
                                                                                                       APPLICATION NUMBER: US/08/463,115 FILING DATE: June 5, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION:
US-08-463-115-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 GGGGGGNC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-465-388-56
```

ò ద

```
2043 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 2102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 AGTGGATCCCCCGGCCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                  Query Match 40.3%; Score 60; DB 3; Length 4164; Best Local Similarity 100.0%; Pred. No. 4.6e-12; Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jef D.
APPLICANT: Braiterman, Lelita T.
APPLICANT: Braiterman, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial TITLE OF INVENTION: Transposons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie, and Beckett
STREET: 1001 G Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASTPICATION:
PRIOR APPLICATION NUMBER: US 08/204,675
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 31,141
RECISTRATION NUMBER: 32,141
RECISTRATION NUMBER: 31,141
RECISTRATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH 4164 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-08-796-364-1
Sequence 1, Application US/08796364
; Patent No. 5968785
       STRANDEDNESS: double
TOPOLOGY: dircular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: # NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cfrcular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                             MATI-SENSE: NC
: IMMEDIATE SOURCE:
: CLONE: PAT-1
US-08-660-754-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NS-08-661754-1

| Sequence 1, Application US/08660754
| Patent No. 58437101
| GENERAL INFORMATION:
| APPLICANT: Boeke, Jef D. APPLICANT: Braiterman, Lelita T. TITLE OF INVENTION: In Vitro Transposition of Artificial TITLE OF INVENTION: Transposons NUMBER OF SEQUENCES: 7
| CORRESPONDENCE ADDRESS: 7
| ADDRESSEE: Banner, Birch, McKie, and Beckett STREET: 1001 G Street, N.W. STREET: 0.S. GOUTRY: U.S.A. STREET: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 40.3%; Score 60; DB 1; Length 4164; Best Local Similarity 100.0%; Pred. No. 4.6e-12; Matches 60; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,754
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTUNDADA, TANGERA, TANGERA, TANGER, SETERA, A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELECOMMUNICATION INFORMATION:
TELEFRONE: 202.508.910
TELEFAX: 202.508.929
TELEFAX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
ATTORNEY/AGENT INFORMATION:
NAME: RAGAN, SATAN A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELECOMMUNICATION INFORMATION:
TELEPAX: 202.508.910
TELEFAX: 202.508.929
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERIFICS:
LENGTH: 4164 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: PAT-1
US-08-204-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
```

0;	9
; Gaps	7 0 4 0 0
0	É
Indels	000
0	000
; Mismatches	
; 0	
Conservative	
60;	
Matches	•
~	ď

Search completed: May 29, 2000, 22:09:10 Job time: 38751 sec

Run on:

```
May 30, 2000, 09:48:31; Search time 2276.24 Seconds (without alignments) 292.062 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GGCCAAAATTGAAAACTA............TTGTTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pending_Patents_NA:*/

| cgnl_6/ptodata/1/pna/PCTUS_COMB.seq:*/
| cgnl_6/ptodata/1/pna/US08_COMB.seq:*/
| cgnl_6/ptodata/1/pna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cgnl_6/ptodata/1/pna/US091A_COMB.seq:
/cgnl_6/ptodata/1/pna/US091B_COMB.seq:
/cgnl_6/ptodata/1/pna/US091C_COMB.seq:
/cgnl_6/ptodata/1/pna/US092A_COMB.seq:
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5142629 seqs, 2230885800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                     US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                 OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
```

cgnl_6/ptodata/1/pna/US092B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US092E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US092E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US092E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US093E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US093E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US093E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US093E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US093E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US093E_COMB.seq:*

(cgnl_6/ptodata/1/pna/US094A_COMB.seq:*

(cgnl_6/ptodata/1/pna/US091A_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001A_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq:*

(cgnl_6/ptodata/1/pna/US001B_COMB.seq: /cgnl_6/ptodata/1/pna/US06_NEW_COMB.seq:*
/cgnl_6/ptodata/1/pna/US07_NEW_COMB.seq:*
/cgnl_6/ptodata/1/pna/US08_NEW_COMB.seq:*
/cgnl_6/ptodata/1/pna/US09_NEW_COMB.seq:*
/cgnl_6/ptodata/1/pna/US06_NEW_COMB.seq:* ptodata/1/pna/US6019_COMB.seq: 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	1 149 100.0 149 28 US-08-935-377-8 Sequence 8, Appli 2 138 92.6 150 28 US-08-935-377-9 Sequence 9, Appli
ID	149 28 US-08-935-377-8 150 28 US-08-935-377-9
80	28
Length	149
Query Match	149 100.0 138 92.6
sult No. Score Match Length DB ID	149
Result No.	77

```
RESULT 2
US-08-935-377-9
                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                         oy.
                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                           Sequence 8570, Ap
Sequence 8570, Ap
Sequence 13627, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Ap
Sequence 10, Ap
Sequence 10, A
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 996, Requence 6, Apr
Sequence 6, Apr
Sequence 6, Apr
Sequence 6, Apr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10,
Sequence 10,
Sequence 10,
                                                                                         Sequence 31,
Sequence 59;
Sequence 19;
                                                                                                                                                                  Sequence 857
Sequence 857
                                       Sequence 4,
Sequence 91
Sequence 91
                                                                             Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
US-08-935-377-6
US-08-937-377-6
US-08-937-377-6
US-08-937-377-6
US-08-937-377-6
US-09-123-191-91
US-09-123-191-91
US-09-123-191-91
US-09-123-191-91
US-09-123-191-91
US-09-123-191-91
US-09-133-1782-8570
US-09-133-782-8570
US-09-133-782-8523
US-09-133-782-8523
US-09-133-782-8523
US-09-133-782-8523
US-09-133-782-8523
US-09-133-782-8523
US-09-133-782-8523
US-09-133-782-8523
US-09-132-1255
US-09-132-1200
US-08-146-935-6
US-08-146-935-6
US-08-146-935-100
US-08-146-935-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
```

```
61 GGGCIGCAGGAATICGAIATCAAGCTIATCGAIACCGICGACCICGAGGGGGGGGCCTAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                    Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C STREET: 1100 New York Avenue, N.W., Suite 600 CITY: Washington STATE: D. C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,377

FILING DATE: 22-SEP-1997

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Elic K

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1821.001000/EKS/CMB

TELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELEFAN: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 149; DB 28; Best Local Similarity 100.0%; Pred. No. 5.9e-40; Matches 149; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TAACTAATTTTGTTTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 TAACTAATTTTGTTTTTGGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 150 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: cDNAUS-08-935-377-9
```

g ò

g à

```
61 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCCTAAC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCC----GTGGATCCCCC 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGAGTGGATCCCCC
                                                                                                            GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: T Cells Specific for Target Antigens and TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITT: Weahington
STATE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 5

US-08-377-383-4

Sequence 4, Application US/08377383

Sequence 4, Application US/08377383

Sequence 4, Application US/08377383

Sequence 4, Application: Mathod of Determining Base Sequence of TITLE OF INVENTION: Mathod of Determining Base Sequence of TITLE OF INVENTION: Nucleic Acid NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSE: Cushman Darby & Cushman STREET: Ninth Floor, 1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 131; DB 28; Length 145;
Pred. No. 6.3e-34;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATIBLE PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLASSIFICATION NUMBER: 36.688
REFERENCE/DOCKET NUMBER: 36.688
REFINENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEDUENCE CHRRACTERISTICS:
LENGTH: 145 base pairs
WYDE: NUMBER: 145 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 TAACTAATTTTGTTTTGTGGGCCCGGCC 145
120 TAACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TAACTAATTTTGTTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 87.9%;
Best Local Similarity 97.3%;
Matches 145; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                   1: D. C.
'RY: USA
20005
                                                                     RESULT 4
US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ĥ
                                                                        ï
                                                                                                                                                                                                                   60 CGGCTGCAGGAATTCCATATCAACCTTATCGATACCGTCGACCTCGAGGGGGGCCTAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCTAAC 119
                                                                                                                                                                                                                                                                    61 CGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATG-GTGGATCCCCC 59
                                                                                                                                             Gaps
                                                                                                                      1 GGCCAAAAATTGAAAAACTAGATCTATTTTTTGCACGCGGCCGCCATGA-GTGGATCCCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGAGTGGATCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 137; DB 28; Length 148;
Pred. No. 6.2e-36;
0; Mismatches 0; Indels
                       Length 150;
                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/935,377

FILING DATE: 22-SEP-1997

CLASSIFICATION: 42-1997

CLASSIFICATION: 42-1997

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K

REGISTRATION NUMBER: 35,688

REFERENCE/DOCKET NUMBER: 1821.001000/EKS/CMB

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFONE: (202) 371-2540

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 148 base pairs

TYPE: NUCLeic acid

STRANDEDMESS: single
                    Score 138; DB 28;
Pred. No. 2.9e-36;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                   121 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                  120 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TAACTAATTTGTTTTTGTGGGCCCGGCC 149
                       92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.3%;
Matches 148; Conservative
                                                                        Matches 149; Conservative
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
STATE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           q
```

ä

4; Gaps

g G ö

```
Sequence 91. Application US/09123912A
| Sequence 91. Application Steven G. |
| GENERAL INFORMATION: |
| APPLICANT: Reed, Steven G. |
| APPLICANT: Wang, Tongtong |
| TILE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER |
| FILE REFERENCE: 210121.45521 |
| CURRENT APPLICATION NUMBER: US/09/123,912A |
| CURRENT FILING DATE: 1998-07-27 |
| PRIOR APPLICATION NUMBER: 09/040,802 |
| PRIOR FILING DATE: 1998-03-18 |
| NUMBER OF SEQ ID NOS: 114 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO 91 |
| LENGTH: 858 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AGIGGAICCCCCGGGCTGCAGGAATICGAIATCAAGCTTAICGAIACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70; DB 18; Length 224;
Pred. No. 2e-13;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: Other nucleic acid Synthetic DNA US-08-693-573-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (711)
OTHER INFORMATION: Where n is a, c, g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             öŗ
FILING DATE: 25-JAN-1995
APPLICATION NUMBER: JF657/1994
FILING DATE: 26-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Thomas G. Wiseman
REGISTRATION NUMBER: 35046
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 GGGGGCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 GGGGGCCTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (570)
OTHER INFORMATION: Where n is a,
NAME/KEY: modified_base
LOCATION: (591)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (664)
OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.4%;
Matches 76; Conservative
                                                                                                                                                                                    TELEFAX: (202)822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Where n
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                    LENGTH: 224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified base LOCATION: (667) OTHER INFORMATION: Where NAME/KEY: modified base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (683)
OTHER INFORMATION: Where
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
US-09-123-912-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AGIGGAICCCCCGGGCTGCAGGAATICGAIAICAAGCTTAICGAIACCGICGACCICGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-08-693-573-4
Sequence 4, Application US/08693573
GENERAL INFORMATION:
APPLICANT: FURAMY, Tadashi,
APPLICANT: FURAMY, Tadashi,
APPLICANT: FURAMY, Tadashi,
APPLICANT: CONTRAINES:
CORRESPONDENCE: 4
CORRESPEE: INVELECTUAL PROPERTY GROUP OF
ADDRESSEE: INVELECTUAL PROPERTY GROUP OF
ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
STREET: Whith Floor, 1100 New York Avenue, N.W.
CITY: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.4%; Pred. No. 2e-13;
Matches 76; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
2 IP: 0.5A
2 IP: 0.005-3918
COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.5 inch, 720Kb storage COMPUTER: IBM PC/XT/AT compatibles
    OPERATING SYSTEM: MS-DOS
    SOFTWARE: WordPerfect 5.1 or ASCII editors
    CURRENT APPLICATION NUMBER: US/08/693,573
    FILLING DATE: 07-AUG-1995
CLASSIFICATION: A35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: Other nucleic acid Synthetic DNA US-08-377-383-4
                                                          ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett, 3.5 inch, 720Kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDERFECT 5.1 or ASCII editors
CURRENT APPLICATION DATA:
                                                                                                                                                                                              CONTENT AFFILICATION NUMBER: US/08/377,383
PELING DATE: 25-JAN-1995
CLASSIPICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: JF6971/1994
FILING DATE: 26-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Glenn J. Perry
REGISTATION NUMBER: 28458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 GGGGGCCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 109 GGGGGCCTAACTAACTAATTTTGTT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/377,383
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 224 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: TELEFAX: ()
```

ŏ g

ò ద gor

ú

g

ρ

ΰ

á

ä

δ

ú

ď

б

g or

ù

ď

ö

δ

ò

ď

占

р

ũ

ğ

ò

ρ

ò

ģ

ö

ρ

ò

ď

占

ь

ပဲ

ö

o, g

a,

ö

ь

ΰ

ģ

```
LOCATION: (777)
OTHER INFORMATION: Where n is a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Where n is a, US-09-221-107-91
                 OTHER INFORMATION: Where n is a,
                                                                 LOCATION: (655)
OTHER INFORMATION: Where n is
                                                                                                                                    LOCATION: (664)
OTHER INFORMATION: Where n 1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (787)
OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n is
                                                                                                                                                                                                                        n 1s
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
                                                                                                                                                                                                                                                                                        n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 1S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (801)
OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                      LOCATION: (683)
OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (792)
OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (794)
OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (809)
OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (817)
OTHER INFORMATION: Where
                                                                                                                                                                                                                     INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base LOCATION: (760)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: modified_base
                                                 NAME/KEY: modified_base LOCATION: (655)
                                                                                                                    NAME/KEY: modified_base
                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                    NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                       modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base LOCATION: (765)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: modified_base LOCATION: (820)
                                                                                                                                                                                                                                                                                                                                                                                          modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                        LOCATION
                                                                                                                                                                                                                                                                                                                                         LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE
                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 ataatctcaccagagattcaacgaattccaccacatggactagtggatccccggggct 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AAAATTGAAAAACTAGATCTATTTATTGCACGCGGCGCCCATGAGTGGATCCCCCGGGCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-221-107-91

Sequence 91, Application US/09221107

Sequence 91, Application US/09221107

GENERAL INFORMATION:

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF LUNG CANCER

FILE REFERENCE: 210121.45562

CURRENT FILING DATE: 1998-12-22

NUMBER OF SEQ ID NOS: 161

SOFTWARE: PATENT WELL OF 1005: 161

SEQ ID NO 91

LENGTH: 958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.6%; Score 69.4; DB 40; Length 858; 76.6%; Pred. No. 4.5e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 GCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEX: modified_base
CCATION: (820)
UCCATION: (820)
US-09-123-912-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c, g or t
                                     占
                                                                                                                                     占
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                     ο
o
                                                                                                                                     ρ
                                                                                                                                                                                                                                        þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρ
                                                                                                                                                                                       ς,
g
                                                                                                                                                                                                                                                                                                                                         o,
                                                                                                                                                                                                                                                                                                                                                                                            c,
g
                                                                                                                                                                                                                                                                                                                                                                                                                                             ς,
9
                                                                                                                                     ò
                                                                                                                                                                                                                                        ú
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ù
                                                               LOCATION: (760)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified_base
LOCATION: (765)
OTHER INFORMATION: Where n is a, c,
NAME/KEY: modified_base
LOCATION: (777)
                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (804)
OTHER INFORMATION: Where n 1s a,
NAME/KEY: modified_base
LOCATION: (809)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (570)
OTHER INFORMATION: Where n is a,
FEATURE:
                                                                                                                                                                                       ď
                                     ď
                                                                                                                                                                                                                                        ď
                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                         ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ą
                                                                                                                                                                                                                                                                                        ฒ่
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Where n is NAME/KEY: modified_base LOCATION: (817)
               LOCATION: (759)
OTHER INFORMATION: Where n is NAME/KEY: modified_base
                                                                                                                                                                                 OTHER INFORMATION: Where n is NAME/KEY: modified_base LOCATION: (787)
                                                                                                                                                                                                                                   INFORMATION: Where n is
                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Where n is NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Where n is NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                     INFORMATION: Where n 1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Where n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 76.6'
Matches 85; Conservative
NAME/KEY: modified_base
                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                     OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
```

ı

ö

ρ

ΰ

占

ь

ΰ

ö

p

ò

ö

ρ

ò

g or

ဖ

```
109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 GGGGGGCC 40
                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-09-072-433-31
                                                                                                                                                                                                                                                              FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                     313 ataatctcaccaggagattcaacgaattccaccacactggactagtggatccccgggct 372
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           313 ataatctcaccaggagattcaacgaattccaccacactggactagtggatcccccgggct 372
                                                                   6 AAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGAGTGGATCCCCCGGGCT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AAAATIGAAAAACTAGAICTAITIAIIGCACGCGGCCGCCAIGAGIGGAICCCCCGGGCI 65
                                     ö
   Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 46.6%; Score 69.4; DB 46; Length 858; Best Local Similarity 76.6%; Pred. No. 4.5e-13; Matches 85; Conservative 0; Mismatches 26; Indels 0
                                                                                                                                       66 GCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 91, Application US/09285479;
GENERAL INFORMATION:
ATPLICANT: Wang, TOORGOOD
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LUNG CANCER;
FILE REFERENCE: 210121.455C3;
CURRENT APPLICATION NUMBER: US/09/285,479;
CURRENT FILING DATE: 1999-04-02;
NUMBER OF SEQ ID NOS: 172;
SEQ ID NO 91;
LENGTH: 858
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69.4; DB 43;
Pred. No. 4.5e-13;
0; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Coschigano, Peter W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: BIOREMEDIATION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Sulte 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/09072433 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)...(858)
CTHER INFORMATION: n = A,T,C or G
US-09-285-479-91
46.68;
Query Match
Best Local Similarity 76.6'
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-09-072-433-31/c
                                                                                                                                                                                                                                            US-09-285-479-91
                                                                   ð
                                                                                                     g
                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
US-60-029-960-595/c

Sequence 595, Application US/60029960

Sequence 595, Application US/60029960

APPLICANT: Charles Kunsch

TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 1649

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPPRATING SYSTEM: MSDOS Version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
45.6%; Score 68; DB 38; I
Best Local Similarity 100.0%; Pred. No. 8.2e-13;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
NAME: Carroll, Peter G.
REGISCRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: 0HU-03344
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 705-8410
TELEPRONE: (415) 97-9338
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/60/029,960 FILING DATE:
                                                                                                                                                                                                                                         STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATORNEY/AGENT INFORMATION:
NAME: BLOOKES, A. Anders
REGISTRATION UNUMBER: 36,333
REFERENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEFRAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 595:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                            LENGTH: 147 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
```

Length 381;

```
Query Match
Best Local Similarity 100.0%; Pred. No. 1.1.
Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                      RESULT 14

2.09-515-694-8570
; Sequence 8570, Application US/09515694
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ojeda, Jesse
Palencia, Servando
Raisi, Fariba
                                                                                                                                                                                                                                                                                                                         APPLICANT: Arterburn, Matthew
APPLICANT: Asghari, Vida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee, Won-Jae
Lomellî, Michelle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Randhwa, Gurpreet
Sahourieh, Hannah
Sidhu, Navjiwan
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cheung, Patrick
APPLICANT: Damavandi, Simin
APPLICANT: Dickson, Mark
APPLICANT: Drake, Jim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engleman, Carrie
Faulkner, Brandy
Fox, Melvin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garcia, Veronica
Giedt, Gretchen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smythe, Ashleigh
Tkach, Joe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kita, David
Kofler, Janette
Labat, Ivan
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac, Radoje
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith, Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lynne
Phuong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nogra, Margie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nguyen, Hong
Nguyen, Linh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leni
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Asghari, VicaPPLICANT: Blun, Linda
                                                                                                                                                           109 GGGGGCC 116
                                                                                                                                                                                           157 ggggggcc 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nguyen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nguyen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                          á
                                                                                                                          셤
                                                                                                                                                               à
                                                                                                                                                                                           d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                              93 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

Sequence 8570, Application US/09332782

Sequence 8570, Application US/09332782

SEQUENCE SET SEQUENCES

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

TITLE OF INVENTION: FROW VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-754C0N1

CURRENT FILING DATE: 1999-06-14

EARLIER APPLICATION NUMBER: US/09/332,782

SERLIER APPLICATION NUMBER: US 09/181,430

EARLIER PILING DATE: 1998-10-28

NUMBER OF SED ID NOS: 21027

SOFTWARE: FESTESCE for Windows Version 3.0

SEQ ID NO 8570

LENGTH: 381
                                                                                                                                                                                                                                                                                                                  Sequence 19113, Application US/09411999
CENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
APPLICANT: Shenk, Michael Andrew
TITLE OF INVENTION: Polynucleotides isolated from plants and
TITLE OF INVENTION: methods for their use.
FILE REFERENCE: 1023U
CURRENT FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 37897
SOFTWARE: FastSEQ for Windows Version 3.0
                                                  ch 45.6%; Score 68; DB 63; Length 157;
1 Similarity 100.0%; Pred. No. 8.3e-13;
68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 54; Length 245;
9.4e-13;
thes 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
45.6%; Score 68; DB
Best Local Similarity 100.0%; Pred. No. 9.4
Matches 68; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; LCCATION: (1)...(381)
; OTHER INFORMATION: n = A,T,C or G
US-09-332-782-8570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pinus radiata US-09-411-999-19130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                   Best_Local Similarity
                                                                                                                                                                                               109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 GGGGGGCC 116
                                                                                                                                                                                                                      33 GGGGGGCC 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1111111
90 ggggggcc 97
                                                                                                                                                                                                                                                                                                          US-09-411-999-19130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 19130
LENGTH: 245
US-60-029-960-595
                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                        Matches
                                                                                                                            ò
                                                                                                                                                                                               ò
                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              අ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  요
                                                                                                                                                           g
```

```
ö
                                                                                                49 AGTGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                           97 agtggatcccccgggctgcaggaattcgatatcaagcttatcgataccgtcgacctcgag 156
                                                     Gaps
                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tulpule, Mukul
APPLICANT: Verna, Ron
APPLICANT: Wender, Ron
APPLICANT: Wachter, Adam
APPLICANT: Wachter, Adam
APPLICANT: Wi, James
APPLICANT: Yim, Kenneth
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 754CTP
CURRENT APPLICATION NUMBER: 05/9515,694
CURRENT FILING DATE: 1999-06-14
EARLIER PILING DATE: 1999-06-14
EARLIER PILING DATE: 1999-06-14
EARLIER FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 21027
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 381
                                                  Indels
DB 49; Le:
1.1e-12;
thes 0;
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                              0; Gaps
                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                        US-00-411-999-13627
Sequence 13677, Application US/09411999
Sequence 13677, Application US/09411999
GENERAL INFORMATION:
APPLICANT: Havukkala, Ilkka
APPLICANT: Brenk, Michael Andrew
TITLE OF INVENTION: Polynucleotides isolated from plants and
TITLE OF INVENTION: methods for their use.
FILE REFERENCE: 1023U
CURRENT APPLICATION NUMBER: US/09/411,999
CURRENT FILING DATE: 1999-10-04
NUMBER OF SEQ ID NOS: 37897
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                         Length 381;
                                                                                                                                             Indels
                                                                                                        Query Match 45.6%; Score 68; DB 57; L
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: May 30, 2000, 09:48:32 Job time: 60182 sec
; NAME/KEY: misc_feature
; LCCATION: (1)...(381)
; OTHER INFORMATION: n = A,T,C or G
US-09-515-694-8570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Eucalyptus grandis
US-09-411-999-13627
                                                                                                                                                                                                                                                                        109 GGGGGGCC 116
                                                                                                                                                                                                                                                       109 GGGGGCCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ggggggcc 69
                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                  δ
                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

90 - 8127 ...
90 - 8128 ...
91 - 8128 ...
92 - 8128 ...
93 - 8121 ...
94 - 8121 ...
95 - 8131 ...
96 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...
97 - 8131 ...

```
May 29, 2000, 21:13:16 ; Search time 2192.43 Seconds (without alignments) 275.462 Million cell updates/sec
                                                                       US-08-935-377-8
149
1 GGCCAAAATTGAAAACTA......TTGTTTTGTGGGCCCGGCC 149
                                                                                                                                          9714632
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                           4857316 seqs, 2026611650 residues
                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                             OM nucleic - nucleic search, using sw model
                                                                                                     IDENTITY_NUC .
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                              em_est10:*
em_est11:*
em_est13:*
em_est14:*
em_est16:*
em_est16:*
                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                  em_est1:*
em_est2:*
em_est4:*
em_est5:*
em_est5:*
em_est7:*
em_est8:*
em_est8:*
                                                                                                                                                                                                            EST: *
                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
Sequence:
                                                                                                     Scoring table:
```

Database :

Searched:

Run on:

gb_est40::*
gb_est41::*
gb_est41::*
gb_est43::*
em_est31::*
em_est33::*
gb_est45::*
gb_est45::*
gb_est45::*
gb_est45::*
gb_gss1::*
em_gss1::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9b_9ss11:*
9b_9ss10:*
9b_9ss10:*
em_9ss10:*
em_9ss11:*
9b_9ss12:*
9b_9ss12:*
9b_9ss14:*
9b_9ss14:*
9b_9ss14:*

em_gss2: em_gss3: em_gss4: gb_gss6: em_gss5: em_gss5: gb_gss7: gb_gss9: gb_gss9: em_gss7:

SUMMARIES

Department of Eukaryotic G The Institute for Genomic 9712 Medical Center Dr., F	Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from	http://www.tigr.org/tdb/ht seq primer: M13-21	Class: BAC ends. FEATURES Location/Qualifie source 1682		/clone="2301Lz3" /clone_11b="CIT-1	/ Sex="male" /cell_type="Speri /note="Vector: pl	Hindlii" BASE COUNT 156 a 187 c 187 ORIGIN	:	Query Match Best Local Similarity 93.7%; Prev	10 CO	Db 79 AGTGGATCCCCGGGGTGCAGGAATTC	OV 109 GGGGGCCTAACTAACTAA 127	19 GGGGGCCCGAGTACCCAA		RESULT 2 AQ009167/c	LOCUS AQ009167 608 bp D DEFINITION CIT-HFP-2281N13.TF CIT-HS	genomic survey sequence. ACCESSION AQ009167			EUKAIYOLG; MCCGZOG; CLOYU Eutherla; Primates; Catar REFERENCE 1 (bases 1 to 608) AOTHORS Adams, M.D., Rounsley, S.D.		AL		Department or Eukaryotic The Institute for Genomic 9712 Medical Center Dr.,	Tel: 301 838 0200  7	Clones are available from end search page:  http://www.itr.org/idb/P	Seq Primer: M13-21; Class: BAC ends.	FEATURES Location/Qualifi source 1608
Description	AQ00463 CIT-HSP-2 AQ009167 CIT-HF9-2 B69688 CIT9768K-A- B54292 CIT-HSP-201	AUU37147 AUU37147 B95279 CIT-HSP-217 B80294 CIT-HSP-204	AQ013255 CIT-HSP-2 AQ041198 CIT-HSP-2 T48593 ph6f4 19/1T	AA052885 73551 Blo B74162 CIT-HSP-202	AQ014512 CIT-HSP-2 B65534 CIT-HSP-202	AQ012629 CIT-HSP-2 AQ012216 CIT-HSP-2 AQ012221 CIT-HSP-2	AQ009165 CIT-HFP-2 B64363 CIT-HSP-202 B70299 CIT-HSP-202	AQ016737 CIT-HSP-2 B68775 CIT-HSP-205	B80296 CIT-HSP-204 AQ009153 CIT-HSP-2	AQU/4695 CIT-HSF-Z AA752172 96B90243	AQUU843/ CII-HSF-2 AQU14519 CII-HSF-2 R720RR CII978SK-13	AQ012365 CIT-HSP-2	B26269 F10B5TF IGF U68746 Riftla bach	A1239372 SWOVAFCAP A0003238 RPC111-19	B53695 CIT-HSP-201 AA752115 96BS0066	B65391 CIT-HSP-202 A1058116 SWAMCAC15	AQ024018 CPGR0359A AQ023564 CPGR0482A	AQ023548 CPGR0051A AQ024077 CPGR0415A	AQ023674 CpGR0007B AQ044029 CIT-HSP-2			GSS 20-AGG-1998 ens genomic clone 2301L23,			ıta; Vertebrata; Mammalla; Inidae; Homo.	Bass, S., Linher, R., Golden, K., C., Shizuya, H., Simon, M. and	nce Database for Sequence-Ready	
ΩI	96 AQ074693 96 AQ009167 84 B69688 84 B54292																			ALIGNMENTS		682 bp DNA 301L23.TF CIT-HSP Homo sapiens	lence. 1811		Chordata; Craniata; Vertebr Catarrhini; Hominidae; Homo	y,S.D., Zhao,S., Bas: )., Suh,E., Wible,C.,	nan BAC End Sequence	
th DB	682 608 528 8,108																					682 b	segu::3436		azoa	ounsle ger,I	my mo	1998) Adams
Query e Match Len	71 47.7 68 69 46.3 60 1.4 45.9 52 68 45.6 10	4 4 4 6 5 6 6 6 6	45.6	4 4 4 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	45.6 45.6	4 4 4 5 5 6 6 6 6	444 70.00	4 4 4 5 70 70 5 9 9	45.6	67 45.0 67 45.0	44.6	42.6	.6 441.3	60 40.3 50 50 50 50 50 50 50 50 50 50 50 50 50 5	. 80 c	57 38.3 8 38 1	37.6	56 37.6 56 37.6	.2 37.0			AQ074693 CIT-HSP-2301L2	genomic survey AQ074693 AQ074693.1 GI	GSS. human. Homo caniens	Eukaryota; Metazoa; Choi Eutheria; Primates; Cat:	<pre>1 (bases 1 to 682) Adams,M.D., Rounsley,S. Berry,K., Granger,D., S</pre>	Venter, J.C. Use of a rando	map building Unpublished (1 Contact: Mark
Result No. Scor	10.64			017		15 16 17	. m. m. c	C	· ·	10.10	28 66		32.	2. A	י מי מי	, w o	, 0 -	100	4.2		RESULT 1	AQ074693/c LOCUS DEFINITION		KEYWORDS SOURCE	\$	REFERENCE AUTHORS	TITLE	JOURNAL

₹

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 om Research Genetics (info@resgen.com). BAC
                                                                                          nm Research Genetics (info@resgen.com). BAC
                                                                                                                             humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D., Field, C.E., Bass, S., Linher, K., anger, D., Suh, E., Wible, C., Kim, U.-J., d Venter, J.C. Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA GSS 27-JUN-1998
HSP Homo sapiens genomic clone 2281N13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rdata; Craniata; Vertebrata; Mammalia;
arrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                              srm"
pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                          ced. No. 8.1e-14;
Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .N13.TR.1 CIT-HSP-2281N13.TF
                                                                                                                                                                                                                                                                                                                                             1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c Genomics
ic Research
, Rockville, MD 20850, USA
Genomics
c Research
Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                           151 t
                                                                                                                                                                                                             sapiens"
1:9606"
                                                                                                                                                                                                                                                                                                                                           37 g
                                                                                                                                                                                                                                                              -HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fiers
                                                                                                                                                                                  iers
```

ö

Gaps

ö

Indels

```
Unpublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: maddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Simon, M., and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
                                                          B54292 108 bp DNA GSS 20-JUN-1998 CIT-HSP-2017M1.TR CIT-HSP Homo sapiens genomic clone 2017M1, genomic survey sequence.
  Pred. No. 5.9e-13;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:7044003"
/db_xref="taxon:9606"
/clone="2017N1"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
  Best Local Similarity 98.6%;
Matches 69; Conservative (
                                                                                                                                                                                                                                                                                                                                B54292
B54292.1 GI:2608626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HindIII"
a 35 c
                                                                                                                                      109 GGGGGGCCTA 118
                                                                                                                                                            16 GGGGGGCCCA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 GGGGGCC 100
                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                셤
                                                                                                                                        ö
                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dipublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdddams@figr.corg
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             869688 528 bp DNA GSS 18-JUN-1998
CIT978SK-A-448E10.TVC CIT978SK Homo sapiens genomic clone A-448E10,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Fibroblast"
/note="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library A"
138 c 147 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata: Vertebrata; Mammalia;
Eutheria: Primates: Catarrhini: Hominidae: Homo.

1 (bases i to 528)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Kim,U.-J.,
Shizuya,H., Simon,M. and Venter,J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                              49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="CDB:1147360"
/db_xref="taxon:9606"
/clone_12281N13"
/clone_11b="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                        Length 608;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                    Query Match
46.3%; Score 69; DB 96; 1
Best Local Similarity 100.0%; Pred. No. 3.8e-13;
Matches 69; Conservative 0; Mismatches 0;
                                                                                                                                                                            137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 528
/organism="Homo sapiens"
/db_xref="GDB:5299607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="A-448E10"
/clone_lib="CIT978SK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                            166 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     869688.1 GI:2708912
                                                                                                                                                                            164 c
                                                                                                                                                                                                                                                                                                                                                                                                         109 GGGGGGCCT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                               23 GGGGGCCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118
                                                                                                                                                                            141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
B69688/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
ö
                                                                                                                                                                                                         49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                    ö
                                                                                                                               Length 108;
                                                                                                                                                                    Indels
                                                                                                                             Query Match
45.6%; Score 68; DB 84; L
Best Local Similarity 100.0%; Pred. No. 6.3e-13;
Matches 68; Conservative 0; Mismatches 0;
                                                        13
                                                      34 9
```

RESULT AU037147

DB 84; Length 528;

45.9%; Score 68.4;

Query Match

4. 4. 4. 4.

us-08-935-377-8.rst

```
Contact: Mark Adams
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
Ditable Madical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: madams@tigr.org
Clones are available from Research Genetics (info@tesgen.com). BAC end search page:
Department Maj Reverse
Seg primer: Mj Reverse
Class: BAC ends.
                                      Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
and search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: Mi3-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49 AGIGGAICCCCCGGGCTGCAGGAAITCGAIAICAAGCITAICGAIACCGICGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B80294 '144 bp DNA GSS 24-OCT-1998 CIT-HSP-2045D19.TR CIT-HSP Homo sapiens genomic clone 2045D19, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
45.6%; Score 68; DB 96; Length 14.
Best Local Similarity 100.0%; Pred. No. 6.5e-13;
Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 35 t

    144
    /organism="Homo sapiens".
    /db_xref="GDB:7054558"
    /db_xref="taxon:9606"

                                                                                                                                                                Location/Qualiflers
1. 141.
/organism="Homo sapiens"
/db_xref="GDB:7103988"
                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="2172N2"
/clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 41 g
                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B80294
B80294.1 GI:2867317
                                                                                                                                                                                                                                                                                                                                                                                                                   41 c
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 GGGGGGCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
B80294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                          Eukaryota: Dictyostellum.

Eukaryota: Dictyostellum.

(bases 1 to 141)

(bases 1 to 141)

(bases 1 to 141)

(bases 1 to 141)

(bases 2 to 141)

(bases 3 to 141)

(bases 3 to 141)

(bases 4 to 141)

(contact: Mizuno, H., Yoshida, M., Yoshida, M., Yoshida, M., Yoshida, M., Yoshida, M., Yoshida, M., Yakenchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y.

Williams, J., Maeda, M., Takeuchi, J., Ochiai, H. and Tanaka, H.,

Williams, J., 1998 this sequence version replaced gi:2153012.

Contact: Hideko Urushihara
  AU037147 141 bp mRNA EST 29-MAR-1999
AU037147 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSB532, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simon, M. and Verter, J.C.
Simon, M. and Verter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:44689"
/clone="SSB532"
/clone_lib="Dictyostellum discoldeum SS (H.Urushlhara)"
/dev_stage="slug"
/dev_stage="slug"
/dev_stage="slug"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B95279 141 bp DNA GSS 26-JUN-1998 CIT-HSP-2172N2.TF CIT-HSP HOMO SAPIENS GENOMIC CLONE 2172N2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Emali: d402hu@akura.cc.tsukuba.ac.jp
PROJECT - 'Dictyostelium discoideum cDNA project in Japan',
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.6%; Score 68; DB 44; Length 14 Best Local Similarity 100.0%; Pred. No. 6.5e-13; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Dictyostelium discoideum'
                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute of Biological Sciences
University of Tsukuba
                                                                                                                                     Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic survey sequence.
B95279
B95279.1 GI:2977616
                                                                                            AU037147.1 GI:3983900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="AX4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 GGGGGCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 namn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
           LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
B95279/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                          ACCESSION
                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                           TITLE
```

ŏ 엄 ò 셤 į

```
109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 GGGGGGCC: 139
                                                                                                                                                        109 GGGGGGCC 11.6
                                                                                                                                                                                          42 GGGGGGCC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                  σ
                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                         AQ041198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
T48593
                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                        ö
                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dubulished (1998)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Exa:: 301 838 0200
Exa:: 301 838 0200
Exa:: Judic Contact Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax:: 301 838 0200
Exa:: Judic Contact Dr., Rockville, MD 20850, USA
Tel:: Judic Contact Dr., Rockville, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 169)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Simon, M. and Yenter, J.C.

Simon, M. and Yenter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   69 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 128
                                                                                                                                                                                                                                                                                                                                                                                                            49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQUI3255 169 bp DNA GSS 06-JUN-1998 CIT-HSP-2299C22,TF CIT-HSP Homo sapiens genomic clone 2299C22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                            Gaps
/clone_12045D19"
/clone_11b-"CIT-HSP"
/sex-"Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                         ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                               Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 45.6%; Score 68; DB 96; Length 169; Best Local Similarity 100.0%; Pred. No. 6.7e-13; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                               Query Match
45.6%; Score 68; DB 84; 1
Best Local Similarity 100.0%; Pred. No. 6.6e-13;
Matches 68; Conservative 0; Mismatches 0;
                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:1154018"
/db_xref="haxon:9606"
/clone="2299c22"
/clone="LT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .169
                                                                                                                                                                                     41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ013255.1 GI:3185820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex-"Male"
                                                                                                                                                                                     43 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GGGGGGCC 136
                                                                                                                                                                                     34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
AQ013255/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dases 1 to 175)

2. Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berryy, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)

Upublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :.
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: MI3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T48593 259 bp mRNA EST 02-FEB-1995 ph6f4_19/ITV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6f4_19/ITV, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ041198 175 bp DNA GSS 14-JUL-1998 CIT-HSP-2335D21.TR CIT-HSP Homo sapiens genomic clone 2335D21, genomic survey sequence.
AQ041198 GI:3310469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Sperm"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 96; L
6.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.6%; Score 68; DB 100.0%; Pred. No. 6.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .175
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="2335D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HindIII"
```

SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

FEATURES

ACCESSION VERSION KEYWORDS

```
/strain="Conde Ad"
/db_xref="taxon:5702"
/clone_lib="Bloodstream form of serodeme ILTatl.1"
/clone_lib="Bloodstream form of serodeme ILTatl.1"
/clone_lib="Bloodstream form of serodeme ILTatl.1"
/note="cond.8" were generated from poly (A+) enriched mRNA
prepared from different developmental stages of T.b.brucei
by reverse transcription followed by PCR amplification
using mini-exon and oilgo(dT) primers. The cDNA generated
were utilized in RADES-PCR coupled with differential
hybridisations to identify differentially expressed mRNA
transcribts. The products which showed to be
differentially expressed were cloned pGEM -T vector.
These differentially expressed mRNA transcripts were (are
being) sequenced to generate differentially expressed
sequence tags."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_GSSS: CIT-HSP-2028N1.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr.: Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 839 0200
Fax: 301 839 0200
Fax: 1 mddams@tigr.cog
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mi3.21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a random BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 386)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B74162 386 bp DNA GSS 24-OCT-1998 CIT-HSP-2028N1.TF CIT-HSP Homo sapiens genomic clone 2028N1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                        /organism="Trypanosoma brucei brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45.6%; Score 68; DB 27; 100.0%; Pred. No. 7.3e-13; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:7048251"
                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
Fax: 254 2 631 499
Email: a.osanya@cgnet.com
Seq primer: M13 primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B74162
B74162.1 GI:2769849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 GGGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
B74162/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="ph64_19/1Tv"
/clone="ph64_19/1Tv"
/clone="bector: pGEM-32; Site_1: EcoR1; Site_2: BamH1; The
library was constructed as described in [Obradovic, D.,
Borodin, A.M., Kopantzev, E.P., Wagner, L.L., Volk, S.V.,
Ermolaeva, O.D., Lebedev, Y.B., Monastyrskaya, G.S.,
Sverdlov, E.D. (1993) Bloorganicheskaya khimia, 20,
919-930]. This protocol is based on nested primer strategy
using Alu-specific primers (ALN3 and TC-65) that direct
the hncDNA synthesis outward of Alu repeats."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 259)
Vinogradova, T.V., Lebedev, Y.B., Kopantzev, E.P., Wagner, L.L., Volik, S.V., Ermolaeva, O.D., Lavrentyeva, I., Monastyrskaya, G.S. and Sverdlov, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA EST 13-SEP-1996 serodeme ILTatl.1 Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 275)
Osanya,A., Murphy,N.B. and Pelle,R.
Trypanosoma brucei brucei cDNAs
Unpublished (1996)
On Nov 29, 1993 this sequence version replaced gi:637578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trypanosoma brucei brucei.
Trypanosoma brucei brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.6%; Score 68; DB 20; Length 259;
100.0%; Pred. No. 7.2e-13;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                              Structure and Function of Human Genes
Shemyakin Institute of Bioorganic Chemistry
Shemyakin Institute of Bioorganic Chemistry
Tal: 70953306529
Fax: 70953306529
Email: sverd@humgen.siobc.msk.su.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unit 3
Livestock Research Institute
Box 30709, Nairobi, Kenya
Tel: 254 2 630 743
                                                                                                                                                                                                                                                                                              Outward Alu-primed hncDNA library
Unpublished (1995)
Contact: Sverdlov ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA052885 275 bp mRNA
T3551 Bloodstream form of serc
brucei cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA052885.1 GI:1543898
EST.
                         GI:642793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 GGGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 GGGGGGCC 122
T48593
T48593.1
                                                                               human.
```

Query Match

Best Loca Matches

ò

요

à 셤

BASE COUNT ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE JOURNAL COMMENT REFERENCE

RESULT 11 AA052885

DEFINITION

ö

Gaps ò

BASE COUNT ORIGIN

Best Loc Matches

ó 硆 ò 셤

```
Outher GSSs: CIT-HSP-2022D24.TR
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
The: 301 838 0200
Fax: 301 838 0208
Email: mddadms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13.21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases: 1 to 519)

Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building
                     49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49 AGTGGATCCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                      GSS 21-JUN-1998
Homo sapiens genomic clone 2022D24,
                                         06-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.6%; Score 68; DB 84; Length 519;
100.0%; Pred. No. 8e-13;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="GD8:7045730"
/db_xref="taxon:9606"
/clone="2022024"
/clone=lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 g
                                                                                                                                                                                                                                                 B65534 519 bp DNA CIT-HSP-2022D24.TF CIT-HSP F genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                                                                                                                                                                                                B65534
B65534.1 GI:2639512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         547 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                     Homo sap∴ens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 GGGGGCC 11.6
                                                                                                      109 GGGGGCC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 a
                                                                                                                                             40 GGGGGCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 GGGGGGCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AQ012629
                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                        RESULT 14
B65534/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
AQ012629
LOCUS
                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                        g
                                                                                                      ò
                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 462)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Li Unpublished (1998)

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                              AQ014512 462 bp DNA GSS 06-JUN-1998 CIT-HSP-2300D21.TF CIT-HSP Homo sapiens genomic clone 2300D21, genomic survey sequence.
AQ014512
AQ014512.1 GI:3184839 GSS.
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                              45.6%; Score 68; DB 84; Length 386; alarity 100.0%; Pred. No. 7.7e-13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 45.6%; Score 68; DB 96; Length 462; Best Local Similarity 100.0%; Pred. No. 7.9e-13; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                               98 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .462
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GDB:7154425"
/db_xref="taxon:9606"
/clone="2300D21"
/clone_lib="CIT-HSP"
/db_xref="taxon:9606"
/clone="2028N1"
/clone_llb="CIT-HSP"
/sex="Male"
                                                                                                                                             109 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hindiii"
a 127 c
                                                                                                                                             98 C
                                                                                                                            HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 109 GGGGGGCC 116
                                                                                                                                                 ø
                                                                                                                                                                                                                                                                                                                                                                                                                                          23 GGGGGGCC 16
                                                                                                                                               81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan.
```

RESULT 13 AQ014512/C LOCUS DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

ö

Gaps

ö

BASE COUNT ORIGIN

FEATURES

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers

1. Gardinal Continuity of the continuity of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 AGIGGAICCCCGGGCTGCAGGAAITCGAIAICAAGCITATCGAIACCGTCGACCTCGAG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
CIT-HSP-2299F1.TR CIT-HSP Homo sapiens genomic clone 2299F1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 45.6%; Score 68; DB 96; Length 547; Best Local Similarity 100.0%; Pred. No. 8.1e-13; Matches 68; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 g
                                                                              AQ012629
AQ012629.1 GI:3185194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154
                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
   DEFINITION
                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δŏ
```

Search completed: May 29, 2000, 21:13:16 Job time: 36515 sec

109 GGGGGGCC 116 ||||||||| 134 GGGGGCC 141

9 6 9

Run on:

```
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45
                                                   May 29, 2000, 21:35:38 ; Search time 1214.87 Seconds (without alignments) 940.489 Million cell updates/sec
                                                                                     US-08-935-377-9
150
1 GGCCAAAAATIGAAAACTA......TIGITTTIGIGGGCCCGGCC 150
                                                                                                                                                                     1765538
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                   882769 segs, 3808571567 residues
                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                   OM nucleic - nucleic search, using sw model
                                                                                                                         IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                      gb_un:*
gb_vi:*
em_fun:*
em_hum1:*
em_hum2:*
em_in:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_vi:*
gb_htgl:*
gb_htg2:*
gb_in1:*
gb_in2:*
em_ba1:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_ba2:*
em_hum3:*
em_hum4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_pr4:*
gb_htg3:*
gb_htg4:*
gb_htg5:*
                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                            9b_bal: *
9b_bal: *
9b_ov: *
9b_ov: *
9b_pal: *
9b_prl: *
9b_prl: *
9b_prl: *
9b_prl: *
9b_prl: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_or:*
em_ov:*
em_pat:*
em_ph:*
em_pl:*
em_ro:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 em_sy:*
em_un:*
                                                                                                                                                                                                                                                    GenEmbl:*
                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                   Database :
                                                                                                         Sequence:
                                                                                                                                                    Searched:
```

```
9b_htg6: *
9m_htg7: *
9m_htg1: *
em_htg2: *
em_htg3: *
em_htg3: *
em_htg3: *
gb_pt5: *
gb_htg9: *
gb_htg9: *
gb_htg1: *
gb_htg1: *
gb_htg1: *
gb_htg1: *
gb_htg1: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	R060142 Seque	٠	ā	ā,	ď,	LO8785 Bluescribe	บั	Plasmi	Yeast in	Plasmi	Yeast	Yeast in	25 pGALL	7 pGA11(	-	Veact Co	Young Y	Clonin	Yeast C	. Cloning	Yeast in	Clonin	Yeast inte		۲.	AJ005323 pCP1(-) K AD001531 Cloning v		Ε;	'l Magna	' Cloning	22848 Clonin	52324 pBluescri	52325 pBluescri	_	52328 pBluescr1	08787 BlueScrib	86	U47947 Cloning vec	7/829 CIONING	332	132 Plasmid pB
SUMMARIES	a	R06014	ARBLKSM	ARBLKSP	ARBL2KSM	ARBL2KSP	SYNELKSBV	SYNPBEN66	XXU35131		XXU35136	PRS306	PRS303	ASAU5326	ASAU5329	AAUU25/4	DRC314	516316	XXU25060	PRS313	CVU23751	034887	XXU25059	PRS305	CV014125	PRSSLO	ASAJ5323 SYNPGR8V	XXU43955	G16589	AF015771	SYNPLKRA	SYNPLKRB	ARBLSKM	ARBLSKP	ARBLZSKM	ARBLZSKP	SYNBLDKPV	SYNBLSKMV	CVU47947	CVE/829	352	13
	BB:	יט	14			14	14				14				7 .						14						14 14	14	13	ω					74				77	T 4	7	14
	Length	7	95	95	96	96	9 6	30	7	26	28	37	44	25	2 6	2 6	2 0	2 0	95	96	14	138	22	20	63	5 ;	4 L	99	5	4	4	14	95	95	96	96	96	96	o o	7	34	35
\$ Query	; t	-:-												٠				•									၀.၀ ဖစ					•	٠	•	٠	٠	7	٠	•	٠	4	. 4
* 3	Ma		4 4			4 -							4		7 -	<del>,</del> -	+ =	7	4						4	4.	4 4	7	4									4.		4	4	4
	Score	9.	6 6	69	69	69	0 6	60	69	69	69	69	69	בי בי	D (	200	0 0	0 0	69	69	69	69	69	69	6 G	י פ	თ თ დ დ	9		•	67	67	67	67	67	67	67	67	67	٥	67	67
sult	No.	<b>~</b> (	N M	4	ı,	φ,	- α	o 0	10	11	175	E :	4.	<u>م</u> ب	1 1	1 -	9 0	25	22	22	23	77	52	56	27	9 0	300	31	32	33	34	35	36	37	38	9	0 1	41	42	5	44	
Resi	- ;		U					υ						υ													υ	U	υ	ပ		υ	U	O	υ	υ	O	O	υ	υ	O	

ALIGNMENTS

```
Direct Submission
Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
2 (bases 1 to 2958)
Short,J.W., Fernandez,J.W., Sorge,J.A. and Huse,W.D.
Lambda ZAP: a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                             Direct Submission
Submitted (20-FEB-1990) Thomas E.A., Stratagene Clonin Systems,
1099 North Torney Pines Rd., La Jolla, CA 92037, USA
(bases 1 to 2958)
Short,J.M., Fernandez,J.M., Sorge,J.A. and Huse,W.D.
Lambda 2AP: a bacteriophage lambda expression vector with in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GIGGAICCCCCGGGCTGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circular SYN 11-JUN-1998
phagemid excised from lambda ZAP
                                                                                              cloning vector; expression vector; vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cloning vector; expression vector; vector
                             circular SYN 10-MAY-1995
phagemid excised from lambda ZAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 14; Length 2958; Pred. No. 2.3e-12; 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
88319944
                                                                                                                                                                                                                                                                                               excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .2958
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .2958
/note="phagemid pBluescript KS(-)"
754 c 731 g 765 t
                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 2958)
Alting-Mess,M.A. and Short,J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARBLKSP 2958 bp DNA
pBluescript KS(+) vector DNA,
X52331
                             ARBLKSM 2958 bp DNA, pBluescript KS(-) vector DNA, X52326 X52326.1 GI:58064
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             747 GGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GGGGGCCTAACTAACTATTTGTT 135
                                                                                            artificial sequence, c
synthetic construct.
synthetic construct
artificial sequence.
(bases 1 to 2958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.2%;
Matches 75; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           artificial sequence;
synthetic construct.
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             artificial sequence.
1 (bases 1 to 2958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 2958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X52331.1 GI:58065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homas, E.A.
                                                                                                                                                                                  homas, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
ACCESSION
                                              DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                               ORGANISM
                                                                                                                                                                                                                                               REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                               MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                KEYWORDS
RESULT
ARBLKSM
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARBLKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unclassified.

1 (bases 1 to 259)
Chandley, A.C., Kun, M., Sharkey, A.M., Hargreave, T.B. and Cooke, H.J., Chandley, A.C., Kun, M., Sharkey, A.M., Hargreave, T.B. and Cooke, H.J., AZOOSPERMIA IDENTIFICATION AND TREATMENT PATENT. WO 9511300-A 9 27-APR-1995;
MEDICAL RES COUNCIL (GB)
Other publication AU 7947794 950508.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                  Length 793;
                                                                                                                                         Unclassified.

Unclassified.

Unclassified.

Unclassified.

St. George-Hyslop,P.H., Rommens,J.M. and Fraser,P.E.
St. George-Hyslop,P.H., Rommens,J.M. and Fraser,P.E.
Nucleic acids encoding presentith II
Patent: US 5840540-A 121 24-NOV-1998;
Location/Qualifiers

1. 793

1. 793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 69; DB 5; Length 255
Pred. No. 1.7e-12;
0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7. 259
/organism="unidentified"
/db_xref="taxon:32644"
/clone_lib="mouse Genomic Library"
/clone="M3.2" 63 g 69 t 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAT
                                    PAT
                                                                                                                                                                                                                                                                                                                                                 Score 69.8; DB 5;
Pred. No. 1.1e-12;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCGACCTCGAGGGGGCCCGGTACCCAGCTTTTGTT 34
                                  AR060142 793 bp DNA
Sequence 121 from patent US 5840540.
AR060142
AR060142.1 GI:5986592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A44281 259 bp DNA
Sequence 9 from Patent WO9511300.
A44281
                                                                                                                                                                                                                                                                   /organism="unknown"
242 c 146 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 GGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGCCCGGTACCCAGCTTTTGTT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 88.2%;
Matches 75; Conservative (
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A44281.1 GI:2299115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
                                                                                                               unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
                                                                                                                                       Unknown
                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
     RESULT 1
AR060142/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                   ACCESSION
VERSION
                                                                                                                                                                                                    TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A44281/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                   KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    å
                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                     ò
```

ö

Gaps

source

JOURNAL MEDLINE FEATURES

REFERENCE AUTHORS TITLE

TITLE JOURNAL MEDLINE

BASE COUNT ORIGIN

```
Direct Submission
Direct Submission
Direct Submission
Direct Submission
Dispersion of Street 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cloning vector; expression vector; vector
                                                                                                                                                                                                                                                                                                                                                       ARBL2KSP 2961 bp DNA circular SYN 10-MAY-1995 pBluescript II KS(+) vector DNA, phagemid excised from lambda ZAPII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="phagemid pBluescriptII KS(+)"
738 c 755 g 721 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.0%; Score 69; DB 14;
ilarity 88.2%; Pred. No. 2.3e-12;
Conservative 0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. 2961
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .2961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alting-Mees, M.A. and Short, J.M.
Alting-Mees, M.A. and Short, J.M.
Ballouscript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        circular
vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYNBLKSMV 2964 bp DNA
BlueScribe KS Minus cloning
L08784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GGGGCCTAACTAACTATTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 GGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                           747 GGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obtained from VecBase 3.0
                                                                                                                                                    111 GGGGCCTAACTAACTATTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequence; osynthetic construct.
synthetic construct
artificial sequence.

[ (bases 1 to 2961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct
artificial sequence.
1 (bases 1 to 2964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L08784.1 GI:310728
                                                                                                                                                                                                                                                                                                                                                                                                                                            X52327
X52327.1 GI:58061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 75; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thomas, E.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ಪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYNBLKSMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                               ARBL2KSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                     요
                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                   (bases 1 to 2958)
Lampe, D.J., Grant, T.E. and Robertson, H.M.
Factors affecting transposition of the Himarl mariner transposon in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (20-FBB-1990) Thomas B.A., Stratagene Clonin Systems,
11099 North Torney Pines Rd., La Jolla, CA 92037, USA
(Dases 1 to 2961)
Short, J.M., Fernandez, J.M., Sorge, J.A. and Huse, W.D.
Lambda Zahs: a bacteriophage lambda expression vector with in vivo
excision properties
Nucleic Acids Res. 16 (15), 7583-7600 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X52329
X52329.1 GI:58060
artificial sequence; cloning vector; expression vector; vector. synthetic construct. synthetic construct artificial sequence. 1 (bases 1 to 2961)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARBL2KSM 2961 bp DNA circular SYN 10-MAY-1995
pBluescript II KS(-) vector DNA, phagemid excised from lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 14; Length 2961;
Pred. No. 2.3e-12;
0; Mismatches 10; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 46.0%; Score 69; DB 14; Length 2958; Best Local Similarity 88.2%; Pred. No. 2.3e-12; Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="phagemid pBluescriptII KS(-)"
758 c 735 g 762 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="phagemid pBluescript KS(+)"
734 c 751 g 724 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .2961
/organism="synthetic construct"
/db_xref="taxon:32630"
1. .2961
                                                                                                                                                                                                                                                                                                                               1. 2958
/organism="synthetic construct"
/db_xref="taxon:32630"
1. 2958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (bases 1 to 2961)
Alting-Mees,M.A. and Short,J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
Alting-Mees,M.A. and Short,J.M.
pBluescript II: gene mapping vectors
Nucleic Acids Res. 17 (22), 9494 (1989)
90067967
                                                                                                                                                                                                           vitro
Genetics 149 (1), 179-187 (1998)
98250682
                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 GGGGCCTAACTAACTATTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      747 GGGGCCCGGTACCCAGCTTTGTT 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 88.2%;
Matches 75; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
```

DEFINITION

RESULT ARBL2KSM LOCUS

셤 ö g ORGANISM

REFERENCE AUTHORS

VERSION KEYWORDS SOURCE

ACCESSION

TITLE JOURNAL

REFERENCE AUTHORS

MEDLINE REFERENCE

JOURNAL TITLE

AUTHORS

JOURNAL MEDLINE

ö

Gaps

ö

26-JUL-1993

BASE COUNT

JOURNAL COMMENT

```
The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lac2 region is on the complementary strand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #parent
vecbase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3,
VecSource(3):bGalKS, GenBank(50):PF1
#brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Stratagene
Polylinker region revised 03-APR-1987 according to Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Obtained from VecBase 3.0
Unpublished (1991)
Unpublished (1991)
Unpublished (1991)
Gibert and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Currator Program.
BlueScribe KS Plus - Cloning vector
ENTRY BLUEKSP
TITLE BlueScribe KS Plus - Cloning vector
DATE 28-JAN-1997
#sequence 02-PEB-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #journal Gene (1987) in press
#citation Sequence data from StrataGene
#comment sequence correction according to Stratagene COMMENT
Obtained from StrataGene on floppy disc.
Revised 02-FEB-1987 by F. Pfelffer:
1409/10 'AT' to 'TA' to match revised sequence of PBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This vector contains the fl origin so that the plus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                             51 GIGGAICCCCCGGGCIGCAGGAAIICGAIATCAAGCTIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                          ö
                                                                                                                                                    Length 2964;
                                                                                                                                                                                          10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYN
                                                                                                                                                 Score 69; DB 14;
Pred. No. 2.3e-12;
0; Mismatches 10,
1. .2964
/organism="synthetic construct"
/db_xref="taxon:32630"
a 756 c 735 g 765 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNBLKSPV 2964 bp DNA circular
BlueScribe KS Plus cloning vector.
                                                                                                                                                                                                                                                                                                                        111 GGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                              747 egggcccggracccagcrrrfgrr 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #sequence 04-MAR-1987
#sequence 03-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VecBase(3):BlueM13p
                                                                                                                                                 46.0%;
ilarity 88.2%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                artificial sequence.
1 (bases 1 to 2964)
Gilbert, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic construct
synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L08785.1 GI:310729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION VB0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
CROSSREFERENCE
                                                                                                                                                                        Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                  ์ ๗
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
SOURCE
ORGANISM
                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
SYNBLKSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The stand shown corresponds to pUC19c. As in the published sequence of pUC19c, The M13mp19 lacz region is on the complementary strand.
                                                                                                                                                                                                                                                                                                               #authors Fernandez J.M., Short J.M., Renshaw M., Huse W., Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KpnI-braII-ApaI-XhoI-SalI-ClaI-HindIII-EcoRV-EcoRI-PstI-
smaI-BamHI-SpeI-XbaI-NotI-XmaIII-BstXI-SacII-SacI SELECTION
                                                                                                                                                                                                                                                                                                                                                 #journal Gene (1987) in press
#citation Sequence data from Stratagene
#comment sequence correction according to Stratagene COMMENT
Cobtained from Stratagene on floppy disc.
Revised 02-FEB-1987 by F. Pfelffer:
1409/10 'AT' to 'TA' to match revised sequence of PBR322
Revised 4-MAR-1987 to match sequence of pUC19 on request
of Stratagene
                         These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Currator Program. BlueScribe KS Minus - Cloning vector #TYPE DNA CIRCULAR ITLE BLUESCHIPE KS Minus - Cloning vector DATE 28-JAN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polylinker region revised 03-APR-1987 according to Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VecBase(3):pUC19, VecSource(3):PromT7, VecSource(3):PromT3, VecSource(3):bGalKS, GenBank(50):PF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This vector contains the fl origin so that the minus strand can be obtained upon fl superinfection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #checksum 1589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           643 start of T7-RNA synthesis
774 (c) start of T3-RNA synthesis
1976-2764 789-1 (c) Ap-R; b-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residue source 3 control 3 d 458 548-5943 phage fl 460-624 236-400 pucl9c 626-645 1-20 T7 promoter 653-760 108-1 (c) BlueKS-polylinker 772-791 20-1 (c) T3 promoter 795-2964 448-2617 pucl9c Conflict (cfl) and Mutations (mut): none PARENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626- 645 1- 20 T7 promoter
653- 760 108- 1 (c) BlueKS-polylinker
772- 791 20- 1 (c) T3 promoter
755-1031 237- 1 (c) pUC19
1032-2964 2686- 754 (c) pUC19
Conflict (cfl) and Mutations (mut): none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VecBase(3):BlueKSp, VecBase(3):BlueSKm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phage fl
puc19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #resistance Ap
#indicator beta-galactosidase
MMARY BlueKSm #length 2964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Features of BlueKSm (2964 bp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
5488-5943
449- 285 (c) E
1- 20
                                                                                                                                                                 #sequence 02-FEB-1987
#sequence 04-MAR-1987
#sequence 03-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           #parent
vecBase(3):BlueM13m
                                                                                                                                                                                                                                                      artificial
                  Unpublished (1991)
                                                                                                                                                                                                               #sequence 03
ACCESSION VB0077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
CROSSREFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          residue
3-458
                                                                                                                                                                                               #sednence
                                                                                                                                                                                                                                                                                                   #number 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *brother
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYLINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #parent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARY
                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARENT
```

FEATURES

```
/translation="MSHIQRETSCSRPRLNSNMDADLYGYKWARDNVGQSGATIYRLY
GKPDARELEKHGKGSYANDYDEWYRLNWITERPEMPLPTIKHTIRTPDDAWLITAIP
GKTAROVLEEYPDGSENIVDALAVELRELHSIPVOKNPFRNSDRYFRLAQAGSMNNGL
VDASDFDDERNGWPVEQVWKEMHKLLPFSPDSVYTHGDFSLDNLIFDEGKLIGCIDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-lactamase"
/protein_id="BAA12825.1"
/db_xref="G1:1345435"
/translation="MRIOHERVALIPFFAAFCLPVFAHPETLVWVKDAEDOLGARVGY
IELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGGEOLGRRIHYSQNDLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cloning vector pBSL159 artificial sequence; vectors.

1 (base 1 to 4144)
Alexeyev.M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omega elements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVGIADRYQDLAILWNCLGEFSPSLQKRLFQKYGIDNPDMNKLQFHLMLDEFF"
complement(2209. .3069)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                /note="derived from Tn903; kanamycin resistance gene"
/citation=[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GIGGATCCCCCGGGCIGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 62
                                                                                                                                                                                                                                                                                                                                                   /product="aminoglycoside 3'-phosphotransferase"
/protein_id="BAA12824.1"
/db_xref="GI:1345434"
disruption by circular DNA in Escherichia colied (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XXU35131 4144 bp DNA circular SYN Plasmid pBSL159 cloning vector, complete sequence. U35131 GI:984907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="amipicillin resistance gene"
/citation=[1]
                                                                                   pben66'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46.0%; Score 69; DB 14;
ilarity 88.2%; Pred. No. 2.3e-12;
Conservative 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       862 t
                                                                                 /organism="Cloning vector
/plasmid="pBEN66"
/db_xref="taxon:47800"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(2209. .3069)
                                                                                                                                                                          /note="T3 promoter"
260. .1075
/gene="kan"
                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    790 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 GGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGGGCCGGTACCCAGCTTTGTT 37
                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cloning vector pBSL159.
                                                                                                                                                                                                                                       260. .1075
/gene="kan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EIGASLIKHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="amp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene-"amp'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         800 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 75; Conserva
        One-step dis
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       854
                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
        TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            XXU35131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYNPBENG6 3306 bp DNA circular SYN 06-FEB-1999 Cloning vector pBEN66 DNA for aminoglycoside 3'-phosphotransferase, beta-lactamase, complete cds. D85525 D85525 GI:1345433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KpnI-DraII-ApaI-XhoI-SalI-ClaI-HindIII-EcoRV-EcoRI-PstI-
SmaI-BanHI-SpeI-XbaI-NotI-XmaIII-BstXI-SacII-SacI SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid; aminoglycoside 3'-phosphotransferase; beta-lactamase. Cloning vector pBEN66 (lab_host:E.coli) plasmid:pBEN66 DNA. Cloning vector pBEN66 artificial sequence; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshihiro Yamamoto, Hyogo College of Medicine, Department of Genetics; Mukogawa-cho 1-1, Nishinomiya, Hyogo 663, Japan (Tel:0798-45-6587, Fax:0798-40-7639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (23-MAY-1996) to the DDBJ/EMBL/GenBank databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 69; DB 14; Length 2964; 88.2%; Pred. No. 2.3e-12; Live 0; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                      643 start of T7-RNA synthesis 774 (c) start of T3-RNA synthesis 1976-2764 789-1 (c) Ap-R; b-lactamase
                                                                 source
5943-5488 (c) phage f1
236-400 pUC19C
1-20 T7 promoter
108-1 (c) BlueKS-polylinker
20-1 (c) T3 promoter
                                                                                                                                                                                                                                                                                                                      T7 promoter
BlueKS-polylinker
                                                                                                                                                                                                                                                                                                                                     653-760 108-1 (c) Biuers-polylinke 772-791 20-1 (c) T3 promoter 755-1031 237-1 (c) pUC19 1032-2964 2686-754 (c) pUC19 Conflict (cfl) and Mutations (mut): none
                                                                                                                                                              795-2964 448-2617 pucl9c Conflict (cfl) and Mutations (mut): none PARENT
        VecBase(3):BlueKSm, VecBase(3):BlueSKp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="synthetic construct"
/db_xref="taxon:32630"
736 c 755 g 723 t
                                                                                                                                                                                                                                                                              phage fl
puci9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             indicator beta-galactosidase
ARY BlueKSp #length 2964
Location/Qualifiers
                                                                                                                                                                                                                                     Features of BlueKSp (2964 bp) residue source
                                              Features of BlueKSp (2964 bp)
                                                                                                                                                                                                                                             3- 458 Source (2964 458 Source (2964 460 624 449-285 (C) pt 626-645 11-20 T7 653-760 108-11 (C) B1/22-791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 GGGGCCTAACTAACTATTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto, Y. and Furuyama, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #resistance Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /ататото, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLYLINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                750 a
                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
SYNPBEN66/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

ö

26-SEP-1995

```
Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hengen, P.N.
                                                                                                                                                                                             1128 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                            source
                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
             REFERENCE
AUTHORS
                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 1:
XXU35136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                /transl_table=11
/function="ampicillin resistance"
/function="ampicillin resistance"
/product=beta-lactamase"
/product=beta-lactamase"
/protein_id="AAC53618.1"
/db_xref="G1:984908"
/furanslation="MSOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
/franslation="MSOHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
/franslation="MSOHFRVALGGAVGRIDSFAPFARGDLVFETTINGGARTHYSQNDLVF
YSPVTEKHLPOGMYVRELCSAAITMSDNTAANLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELNEAIPNDERDTHWYAMMATTLRKLLIGEELLILASSROQLIGMAEDKYAGPL
DRWEPELNEAIPNDERDTHWYAMMATTLRKLLIGEELLILASSROQLIGMAEDKYAGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mekkingytyvdisowhrkehfbafosvaoctyngyvolditaf
lktykknkhkrypaffhilarlanahpefrmamkdgelvimdsvhpcytvfhegteff
sslwseyhddfrofihiysodvacygenlayfpkgfienmffvsanpmysfisfdlnv
anmdnffafvftmgkrytyggbkvlmflaiqvhhavcdgfhygrmlnelqqycdefwgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIXTTGSQATMDERNRQIA
                                                                                          (bases 1 to 4144)
Hengen, P.N.
Direct Submission
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Submitted (31-AUG-1995) Paul N. Hengen, Laboratory of Mathematical
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
1 Location/Qualifiers
1 . 4144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cloning vector pRS304.
Cloning vector pRS304
artificial sequence; vectors.
1 (bases 1 to 4267)
Sikorski, R. S. and Heter, P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2726 GIGGAICCCCCGGGCIGCAGAAITCGAIAICAAGCITAICGAIACGGIGGACGICGAGG 2785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRS304 4267 bp DNA circular SYN 14-SEP-1995
Yeast integrative vector pRS304 with TRP1 marker, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 14; Length 4144; Pred. No. 2.3e-12; 0; Mismatches 10; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
/product="chloramphenicol acetyltransferase"
/protein_id="AAC53619.1"
/db_xref="G1:984909"
for Escherichia coli vector construction and in vitro deletion/insertion mutagenesis effor (1), 63-67 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(3704. .4144,1. .219))
                                                                                                                                                                                                                    pBSL159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ų
                                                                                                                                                                                                                  /organism="cloning vector pf
/plasmid="pBSL159"
/db_xref="taxon:4704"
complement(1129: 1989)
/EC_number="3.5.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2786 GGGGCCCGGTACCCAGCTTTTGTT 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       959 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GGGGCCTAACTAACTATTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
U03436
U03436.1 GI:416305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1009 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Si
Matches 75;
                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          디
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                     TITLE
JOURNAL
                                                             JOURNAL
MEDLINE
                                                                                                  REFERENCE
                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
PRS304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
/product="neomycin phosphotransferase"
/product="neomycin phosphotransferase"
/protein_id="aAc53629.1"
/db_xref="G1:984924"
/db_xref="G1:984924"
/translation="MIEQDGLHAGSPAAWVERLEGYDWAQQTIGCSDAAVFRLSAQGR
/translation="MIEQDGLHAGSPAAWVERLEGYDWAQDTIGCSDAAVFRLSAQGR
PVLFVKTOLSGALNEGODEAARLSWLATTGVPCAAVLDVVTEAGRDWLLLGEVPGQDL
LSSHLAPAERVSIMADAMRRHHTLDPATCPFDHQAKIRIERARTRWEAGLVDQDDLDE
ESHGLAPAERFRALKARNPGEDLVVTHGDACLPNINVENGFSGFIDCGRLGVADRY
GDIALATRADIABELGGEWADARTVLYGIAAPDSQRIAFYRLLDEFF"
complement(3301. 4161)
//EC_number="3.5.2.6"
                                               Direct Submission
Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (31-M06-1995) Paul N. Hengen, Laboratory of Mathematical
Biology, National Cancer Institute, Frederick, MD 21702-1201, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cloning vector pBSL97.
Cloning vector pBSL97.
artificial sequence; vectors.
I (bases 1 to 4289)
Alexeyev.M.F., Shokolenko,I.N. and Croughan,T.P.
Improved antibiotic-resistance gene cassettes and omega elements for Escherichia coli vector construction and in vitro delation/insertion mutagenesis
Gene 160 (1), 63-67 (1995)
99354958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1921 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 1980
                                                                                                                                                                                                                                                                                                                                                                                                                                         GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                Length 4267;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  XXU35136 4289 bp DNA circular SYN
Plasmid pBSL97 cloning vector, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
/function="ampicillin resistance"
/product-beta-lactamase"
/protein_id="AAC53630.1"
/db_xref="G1:984925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Cloning vector pRS304"
/db_xref="taxon:31827"

965 c 1092 g 1082 t
                                                                                                                                                                                                                                                                                                                                          Score 69; DB 14; L. Pred. No. 2.3e-12; 0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref-"taxon:42709"
complement(804. .1598)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GGGGCCTAACTAACTATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                  46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 4289)
2 (bases 1 to 4267)
Stillman, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U35136
U35136.1 GI:984923
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
```

```
2167 GGGGGCCGGTACCCAGCTTTGTT 2191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GGGGCCTAACTAACTAATTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="glts"
/codon_start=1
                                                                                                                                                             2 (bases 1 to 4443)
Stillman, D.J.
 U03435.1 GI:416304
                                                                                                                                                                                                                                                                                                            1149 a
                                                                                                                                                 89276910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
ASAJ5326/c
                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
FEATURES
                                                                                       AUTHORS
TITLE
                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                  JOURNAL
                                                                                                                                                             REFERENCE
                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132, USA
Location/Qualifiers
             IELDLNSGKILESFRPEERFPMASTFKVLLCGAVLSRIDAGOEGLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFHHNMGHHYTRL
DRWEPELNEAIPNDEROTTMPVAMATTLRKLLTGELLTLASROOLIDWAEADKVAGPL
LRSALPAGURIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"

1111 g 997 t
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
 'translation-"MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning vector pR3306
artificial sequence; vectors.

1 (bases 1 to 4373)
Sikorski,R.S. and Hieter,P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2015 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 2074
                                                                                                                                                                                                          51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                       14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                        PRS306 4373 bp DNA circular SYN 14-SEP-19
Yeast integrative vector pRS306 with URA3 marker, complete
sequence.
                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4373;
                                                                                                                                              Length 4289,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rmosus 4443 bp DNA circular SYN
Yeast integrative vector pRS303 with HIS3 marker,
U03435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Cloning vector pRS306"
/db_xref="taxon:31829"
| 987 c 1106 g 1099 t
                                                                                                                                              Score 69; DB 14;
Pred. No. 2.3e-12;
0; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69; DB 14;
Pred. No. 2.4e-12;
0; Mismatches 10
                                                                                                                                                                                                                                                                                  2075 GGGGCCCGGTACCCAGCTTTGTT 2099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGGCCCGGTACCCAGCTTTTGTT 2111
                                                                                                                                                                                                                                                                 111 GGGGCCTAACTAACTATTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 GGGGCCTAACTAACTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning vector pRS306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.0%;
88.2%;
                                                                                                                                               Query Match
Best Local Similarity 88.2%;
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 4373)
Stillman, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                             U03438.1 GI:416307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.2
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sonrce
                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRS303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                     g
G
                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                           ò
```

```
Stillman, v. bubmission
Submitted (10-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ?
Cloning vector pRS303.
Cloning vector pRS303
artificial sequence; vectors.
1 (Dases 1 to 4443)
Sikorski, R.S. and Hieter, P.
A system of shuttle vectors and yeast host strains designed for efficient manipulation of DNA in Saccharomyces cerevisiae
Genetics 122 (1), 19-27 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-APR-1998) Gal J., Institute for Biotechnology, Bay
Zoltan Foundation for Applied Research, Szeged, Derkovits fasor
6726, HUNGARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 4670)
Gal,J., Szekeres,S., Schnell,R., Pongor,S., Simoncsits,A.
Kalman,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASAJ5326 4670 bp DNA circular SYN 08-FEE pGAII(+) KS positive selection cloning vector gltS gene. AJ005326 AJ005326.1 GI:4028984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A positive selection cloning system based on the gltS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 46.0%; Score 69; DB 14; Length 4443; Best Local Similarity 88.2%; Pred. No. 2.4e-12; Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Cloning vector pRS303"
/db_xref="taxon:31826"
1 1048 c 1109 g 1137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                construct'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_table=11
/product="glutamate permease"
/protein_id="CAA06473.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli
Anal. Biochem. 266 (2), 235-238 (1999)
99107575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. 4670
/organism="synthetic con/db_xref="taxon:32630"
852. .231
/gene=gits"
852. .2231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              glts gene; glutamate permease. synthetic construct. synthetic construct artificial sequence.
```

```
/db_xref="G1:4028985"
/translation="MEHLDTLATLVAATLTLLLGRKLVHSVSFLKKYTIPEPVAGGLL
/translation="MEHLDTLATLVAATLTLLLGRKLVHSVSFLKKYTIPEPVAGGLL
VALALLVLKKSMGWEVNFDMSLRDPLMLAFFATIGLNGAAWSKLFIERGGRVVGTFLIVVV
GLLVMONAGIGGRAASLIGLDPLMAGLLAGSTILSGGHGTGAAWSKLFIERGGFVANTEV
AMACAFGLVLGGLIGGPVARQLTLFKGNKSWVPGPSRSTVYSISLISNSCSFGDPLV
LERPPPRWSSNSPYSESYTARYLVKHSTTPNGIPDDQEVPTAFEKPDVGRMITSLVLI
ETIALIAICLTVGKIVAQLLAGTAFELPTFVCVLFYGVILSNGLSIMGFYRVERRAVS
VLGNYSLSEFLAMALMGLKIMFLASIALPMLAILVVQTIFMALYAIFVTWRMGKNYD
AAVLAAGHCGFGLGATPTAIANMQAITERFGPSHMAFLVVPRWYGAFFIDIVNALVIKL
YLMLPIFAG"

40 a 1165 c 1231 g 1234 t
                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                        Query Match
46.0%; Score 69; DB 14; Length 4670;
Best Local Similarity 88.2%; Pred. No. 2.4e-12;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 GGGGGCCTAACTAACTATTTGTT 135
                                                                                                                                                                                                                                                                   1040 a
                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
```

Search completed: May 29, 2000, 21:35:42 Job time: 36874 sec

· · ·

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM nucleic - nucleic search, using sw model

May 29, 2000, 21:58:33 ; Search time 1446.77 Seconds (without alignments) 25.940 Million cell updates/sec Run on:

US-08-935-377-9 150 1 GGCCAAAATTGAAAACTA.....TTGTTTTGTGGGCCCGGCC 150 Title: Perfect score:

Sequence:

Scoring table:

311585 seqs, 125096042 residues IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched:

623170 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

N_Geneseq_36:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

(TES		Description	Mouse azoospermia	Nucleotide analogu	Polynucleotide seq	u	Human endogenous	Human endogenous	Plasmid pG+host4	Human steroidogen	Plasmid pG+host5	Plasmid pG+host6	Maize fluory2 gen	Swedish-FAD APP ta	APP t	Swedish/London-FAD	Swedish-FAD APP71	-	fema.		Plasmid pR	iotin D	4	4 Sed	312	4 Sed	Human endogenous	virus		ld pAT-1	2		Nucleotide sequenc	ologo with
SUMMAKIES		ឧ	987664	8	X20513	V31294	T75006	T75005	048463	T39485	048464	048465	V09028	X24730	X24731	X24732	X24733	v68808	V57377	026664	T43794	x02800	X02814	X02815	X02812	X02813	T75010	V10190	V12003	T04575	V22271	V69740	X05602	370015
		图	7	-	Н	-	~	Н	7	Н	ч	٦	7	-	٦	-	-	~	-	Н	-	П	-	٦		-	Н	٦		-	٦	Н	Н	-
		Length	259	501	651	752	1091	1122	3792	4226	5234	6722	10529	12814	15692	15692	15701	545	9629	2640	5356	84	3465	3481	3794	3810	545	.685	685	4164	4164	4164	1949	5170
ď	Query	Match	46.0	46.0	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	44.7	•	44.7	44.7	•	4.	43.9	ë.	•	43.3	•	ω.	43.3	ω.		41.6	÷	ď.	6.	ö	38.8	000
		Score	69	69	67	67	67	67	67	67	67	67	67	67	67	67	67		65.8	S.	ď.	65	65	65	65	φ	m.	62.4	62.	ß	29	'n	58.3	Q U
	ų		7	~	m	4	'n	9	_	<b>&amp;</b>	٥	0	_	~	m	4		y Q	7	80	σ	0		~	m	4	Ŋ	بو	7	z œ	<u>ق</u>	0	-	r
	Result	8	υ				υ					0	-	_	-1	-	7	c J	-	o	_	7	~	~	0	Cł	~	7	7	7	7	e	m	

엄 ò g T04866 standard; DNA; 501 BP. T04866;

RESULT 2 T04866 ID T04866

Candida CaRhol gen Clone #4 from muta E. coll biotin DNA Yeast checkpoint c Yeast RAD17 coding Plasmid pPK13/14 D Plasmid pPK13/14 D Plasmid pPK9/10 DN Plasmid pPK9/10 DN Plasmid pPK7/8 DNA S. aureus MurF ORF DNA sequence of ex	ALIGNMENTS  RESULT 1  887664  887664  887664  887664  887664  888764  8888-1996 (first entry)  8891-1994 (first entry)  8	tch  13 Similarity 88.2%; Pred. No. 8.5e-16; 15 Conservative 0; Mismatches 10; Indels 0; Gaps 0;  GIGGATCCCCCGGGCTGCAGAATTCGATATCATATCGATACCGTCGACCTCGAGG 110
T92869 X027290 X027290 X027290 X01271 V64258 V64255 X29498	ALI 10 gen 11 in in in at in	Score Pred. ); Mis TTCGATA
#>X#X>>>>	BP.  AAZE)  AAZE)  ABBE I  ABBE I  COLET  ABBE I  COLET  ABBE I  ABBE	SC Py O; LATTC
аннапнапнан	(A) (A) (B) (B) (B) (B) (B) (B) (B) (B) (B) (B	08; 28; 1669 1669
3198 459 2150 2150 2973 3956 4088 4583 1094	d; DNA; 259 BP.  first entry) mag factor (AZF) gene ctor; AZF; male infer NA recognition motif End are and infer note = "base n at p in the specificatio elgy = b /*tag = b in the specificatio elgy = b /*note = "base n at p in the specificatio elgy = b /*tag = b in the specificatio elgy = b /*tag	46.0%; larity 88.2%; Conservative :CCCCGGCTGCAGGA. 
$\omega$	d, b d d d d d d d d d d d d d d d d d d	rit CCG CCG
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	standard; DNA;  1996 (first e zoospermia fac rmia factor; A cosme; Rtan  Locat Locat ference 174 fote 1095. 1995. 1994; GB-02186 1994; GB-02186 MEDICAL RES C VAC Cooke H TO T	th Similarity 75; Conser GGATCCCCGG
გი 7. ბი 7. ზი ზი ზი ზი ზი ზ. ზი	e do contract of the contract	h S1 75; 668 668
νο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο ο	RESULT 1 087664 standard 087666 standard 087666 standard 087666 standard 087666 standard 087666 standard 087666 standard 087661 standard 08766	Ma Loc les 51
00000004444444444000000000000000000000	WOODSAARE E SACOCOSA SECULOS SECUES SECULOS SECUES SECUES SECUES SECULOS SECUES SECU	Query M Best Lo Matches 51
000	SECOND BY A MAN WE WE WE WANTED TO SECOND SE	OM W CO

ö

Ë

```
PF 21-NOV-1997; U21347.

PR 14-OCT-1997; US-061953.

PR 22-NOV-1995; US-061953.

PR 22-NOV-1996; US-031626.

A (UVML-) HUMAN GENOME SCI.

A (HUMA-) HUMAN GENOME SCI.

FOI GHOUGH-) UNIV WISCONSIN.

PI (A) Dillon PJ, Welch RA;

New isolated uropathogenic E. coli nucleotide sequences - used to per develop products for the detection of pathogenic E. coli and to products for the detection of pathogenic E. coli and to products for the detection of pathogenic E. coli and to clinit an immune response to pathogenic E. coli and to productly island (PAI) sequences, and represents a nucleic acid pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIS are large fragments of DNA which comprise conclude of the invention. PAIS are large fragments of DNA which comprise conclude of the invention are taken from pathogenicity determinants. The sequences of the invention are taken from the E. coli chromosome and is special approximately 16 who in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in wists to detect uropathogenic E. coli. The proteins are used in vaccines to elicit a protective immune response in an aimal to the uropathogenic E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1998 (first entry)
E. coli J96 pathogenicity island contig #108.
E. coli J96 pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheV; vaccine; protective immune response; ds.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 GIGGAICCCCCGGGCTGCAGGAATICGATAICAAGCTTAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                           GIGGAICCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         775006 standard; DNA; 1091 BP.
775006;
6.0CT-1997 (first entry)
Human endogenous retroviral sequence 6.
Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.7%; Score 67; DB 1; Length 752;
100.0%; Pred. No. 6.5e-15;
.ive. 0; Mismatches 0; Indels
                                                                                                     Length 651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 G;
                                                                                                                 DB 1; Le
6.2e-15;
:
152
                                                                                                             44.7%; Score 67; DB 100.0%; Pred. No. 6.2 iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 C;
    ວີ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V31294 standard; DNA; 752 BP. V31294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.78;
        Ä
                                                                                                         Query Match
Best Local Similarity 100.0
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Conservative
    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 752 BP;
        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 GGGGGCC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 GGGGGCC 6
        651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                      111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT (V31294/C) (V31294/C) (V31294/C) (V31294/C) (V3129/C) (V312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T75006/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEDAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ð
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reeve MA, Robinson PS;

WPI; 95-328290/42.

Reeve MA, Robinson PS;

WPI; 95-328290/42.

Resve MA, Robinson PS;

Wolfication of residual fluorescence labelled nucleotide analogues - to prevent migration in electrophoretic sequencing gel and interference with base calling of DNA chains.

Example: Fig 1; 18pp; English.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 99-081273/07.

New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis Claim 1; Page 257; 1150pp; English.

X20500-2143 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GIGGAICCCCGGGCTGCAGGAAIICGATAICAAGCTIAICGAIACCGICGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28^4MaN-1996 (first entry) Nucleotide analogue treated with calf intestinal alkaline phosphatase. Nucleotide analogue, alkaline phosphatase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X20513;
72-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
Treponema pallidum.
Treponema pallidum.
W09859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.0%; Score 69; DB 1; Length 501
88.2%; Pred. No. 1.1e-15;
ive 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                       /*tag= a
/note= "std. IUPAC codes used"
                                                                                                                                                                          Location/Qualifiers
1. .501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GGGGCCTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 GGGGCCCGGTACCCAGCTTTTGTT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-DEC-1998.
23-UUN-1998; U13041.
24-UUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
Fraser CM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X20513 standard; DNA; 651 BP.
                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1995,
07-MAR-1995; G00490.
08-MAR-1994; EP-301636.
(AMSH ) AMERSHAM INT PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 75; Conserv
                                                                                                                                                                                                                           misc_feature
                                                                                                                                                  Synthetic.
```

RESULT X20513

ò 셤 ŏ g

DOT NAME OF THE PARTY OF THE PA

Gaps

; 0

```
New bacterial plasmid contg. heat sensitive replication system -
and marker gene, opt. capable of chromosomal integration, used to
inactivate specific gene or introduce heterologous gene
Example 2: Fig 9; 73pp; French.

Example 2: Fig 9; 73pp; French.

C Plasmid pGK12 (Appl Environ.Microbiol., 48; 726 (1984)) contg. two
antibiotic resistance marker genes was subjected to mutagenesis with
hydroxylamine. A heat-stable mutant was isolated (coding for a heat-
c sensitive RepA - see Q48466 and Q48467), cut with ClaI and HpaII and
the 334pp Franch lacking the Cm resistance gene was ligated to a
445bp PvuII fragment lacking the Cm resistance gene was ligated to a
445bp PvuII fragment of pBluescript SK+ containing a multicloning
c site, T7 and T3 promoters and sequencing primer binding sites. The
resulting plasmid was designated pVE6004 (or pG+host4 - Q48463). It
is thermosensitive in all hosts tested, including E.coli, and must be
maintained at 28 GGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-1996.
22-MAR-1995 U03396.
23-MAR-1995; US-410540.
(REGC ) UNIV CALIFORNIA.
(UYPE-) UMIV PENNSYLVANIA.
Lin D, Miller WL, Strauss JF;
WPPI; 96-443130/44.
Isolated human steroidogenesis acute regulatory protein gene - used
                                                                                                                                                                                                                                                                 18-MAR-1994 (first entry)
Plasmid pc+host4 containing Ts replication system.
Temperature sensitive replication; antibiotic resistance marker gene
site-specific recombination; chromosomal integration; inactivation;
heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human steroidogenesis acute regulatory protein genomic DNA.
Human; steroidogenesis; acute regulatory protein; hStAR; analysis;
mutation; detection; prenatal; genetic defect; congenital; protein;
lipoid adrenal hyperplasia; treatment; prevention; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 44.7%; Score 67; DB 1; Length 379
Best Local Similarity 100.0%; Pred. No. 1.1e-14;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replacement therapy; hypercholesterolaemia; ds. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                hete...
Synthetic.

// Woo318164-A.

// 16-SEP-1993.
// 12-MAR-1993; FR-003034.

// PR 13-MAR-1992; FR-003034.

PR 13-MAR-1992; FR-003034.

// NRG // INRA INST NAT RECH AGRONOMIQUE.

// Truss A, Maguin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1249 A;
                                                                                                                                                                                                           Q48463 standard; DNA; 3792 BP.
Q48463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T39485 standard; DNA; 4226 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3792 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3481 GGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GGGGGCC 117
111 GGGGGCC 117
                                                      48 GGGGGC
                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endogenous human tumour-associated retroviral element, B18Ag1 - used for the prognosis, diagnosis and monitoring of human cancers, especially breast cancer 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                              Endogenous human tumour-associated retroviral element, B18Ag1 - used
                                                                                                                                                                                                                                    for the prognosis, diagnosis and monitoring of human cancers, especially breast cancer claim 10; Page 31-32; 74pp; English.

Claim 10; Page 31-32; 74pp; English.

Human endogenous retroviral sequences 10, 11-29, 3, 6, 12, 13, 14 and 11-22 (775003-10) were obtd. by screening human genomic libraries using human breast tumnour-associated retroviral element BIBAg1 (see also 775002) as probe. These non-contiguous sequences 11e in order 11-22, 14, BIBAg-1, 13, 12, 10, 3, 11-29, 6 in the retrovirus genome (see also 775001). BIBAg1 and the other retroviral sequences can be used in genetic vaccines and for the prognosis, diagnosis and monitoring of human breast cancer.

Sequence 1091 BP; 79 A; 350 C; 97 G; 248 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human endogenous retroviral sequence 3.
Breast cancer; tumour; B18Ag1; prognosis; diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 44.7%; Score 67; DB 1; Length 109
Best Local Similarity 100.0%; Pred. No. 7.4e-15;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.7%; Score 67; DB 1; L 100.0%; Pred. No. 7.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T75005/c
ID T75005 standard; DNA; 1122 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JAN-1997; U00398.
10-JAN-1996; US-587329.
(CORI-) CORIXA CORP.
Frudakis IN, Smith JW;
WPI: 97-384982/35.
                         10-JAN-1997; U00398.
10-JAN-1996; US-587329.
(CORI.) CORIXA CORP.
Frudakis TN, Smith JM:
                                                                                                                                               Frudakis TN, Smith JM; WPI; 97-384982/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human retrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 GGGGGCC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       409725431-A1.
```

മ

ò 셤 ö g ð d

ö

ö

Length 3792;

1249 T;

742 G;

```
6411 GGGGGCC 6405
                                                                                                                                 bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       업
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                         ğ
88888888888
                                                                                                                                                                                                                                                                                                                                                                                                          ö
  for detection of mutation(s) of this gene that cause congenital lipoid adrenal hyperplasia

C claim 1, Pages 23-25, 89pp; English.

C craulatory protein (hStAR). The hStAR gene can be analysed for regulatory protein (hStAR). The hStAR gene can be analysed for mutations to detect (e.g. prenatally) genetic defects associated with congenital lipoid adrenal hyperplasia (CAH), or its transmission to children. CAH can be treated by protein or gene replacement therapy, which can also be used to prevent or treat hyperrolesterolesterolasmia.

C human adrenal cortex cDNA library was screened with a mouse StAR probe to isolate a 1.6 kb insert, including an ORF for a 285 probe to isolate a 1.6 kb insert, including an ORF for a 285 costiue protein. When it was cloned into pSPORT and expressed in cell collis cotransfected with pP450scc abd pADX, it increased the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pregnenolone synthesis from cholesterol or 1144 processed the level of pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid pd+host5 containing Ts replication system.
Temperature sensitive replication; antibiotic resistance marker gene; site-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bacterial plasmid contg, heat sensitive replication system - New bacterial plasmid contg, heat sensitive replication, used to inactivate specific gene or introduce heterologous gene brample 2; Fig 10; 73pp; French.

Example 2; Fig 10; 73pp; French.

Plasmid pGK12 (App) Environ.Microbiol., 48; 726 (1984)) contg. two antibiotic resistance marker genes was subjected to mutagenesis with hydroxylamine. A heat-stable mutant was isolated (coding for a heat-sensitive RepA - see Q48466 and Q48467), cut with Clai and Hpall and the 3340bp fragment lacking the CM resistance gene was ligated to a 445bp PvulI fragment of pBluescript SK+ containing a multicloning
                                                                                                                                                                                                                                                                                                                                                                                                                                              51 GTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            ö
mutation(s) of this gene that cause congenital
                                                                                                                                                                                                                                                                                                               984 T;
                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 4226;
1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note- "origin of replication from pBR322"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
/note= "from pGK12 (derived from pWV01)"
4384. .4786
                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                               1144 G;
                                                                                                                                                                                                                                                                                                                                                                      44.7%; Score 67; DB 100.0%; Pred. No. 1.2; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                 1132 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1992; FR-003034.
(INRG) INRA INST NAT RECH AGRONOMIQUE.
Gruss A, Maguin E;
WPI; 93-303478/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= c
note= "from pUB110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/standard_name= ORI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
36. .1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= d
/note= "from pSK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9 048464/C

1D 048864 standard; DNA; 5234 BP.

AC 048464;
                                                                                                                                                                                                                                                                                                                   940 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .5234
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.C
Matches 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1993.
12-MAR-1993; F00248.
                                                                                                                                                                                                                                                                                                                   4226 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4209 GGGGGCC 4215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09318164-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qα
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

```
New Part 34-34-84.

New bacterial plasmid contg. heat sensitive replication system and marker gene, opt. capable of chromosomal integration, used to an marker gene, opt. capable of chromosomal integration, used to marker gene, opt. capable of chromosomal integration, used to mactivate specific gene or introduce heterologous gene.

Disclosure, Fig 11; 73pp; French.

Disclosure, Fig 11; 73pp; French.

Cantibiotic resistance marker genes was subjected to mutagenesis with hydroxylamine. A heat-stable mutant was isolated (coding for a heat-sensitive Reph. see Q48466 and Q48467), cut with Clai and Hpall and the 3340bp fragment lacking the Cm resistance gene was ligated to a thing plasmid was designated pVE6004 (or pG+host4 - Q48463).

Cresulting plasmid was designated pVE6004 (or pG+host4 - Q48463).

Cresulting plasmid was designated pVE6004 (or pG+host4 - Q48463).

Cresulting the origin of replication and the ampicillin resistance gene) was inserted into Nail-cleaved, blunt-ended pG+host4 to give pG+host6 (Q48466).The pBR322 ORI allows maintenance of the plasmid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCIIATCGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E.coli at 37 deg.C. while the heat-sensitive ORI allows maintenance at 28 deg.C in gram-positive bacteria.
Sequence 6722 BP; 1961 A; 1278 C; 1503 G; 1980 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 MAR-1994 (first entry)
Plasmid pG+host6 containing Ts replication system.
Plasmid pG+host6 containing Ts replication; entibiotic resistance marker generamerature sensitive replication; antibiotic resistance marker genesite-specific recombination; chromosomal integration; inactivation; heterologous gene expression; thermosensitive plasmid; ds.
site, T7 and T3 promoters and sequencing primer binding sites. The resulting plasmid was designated pVE6004 (or pG+host4 - Q48463). To facilitate cloning in E.coli, the 1.4kb AvaI-AhwNI fragment of pBT322 (containing the origin of replication) was inserted into NSII-cleaved pG+host4 to give pG+host5 (Q48464). The pBR322 ORI allows maintenance of the plasmid in E.coli at 37 deg.C. while the heat-sensitive ORI allows maintenance at 28 deg.C in gram-positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                          1559 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6722;
                                                                                                                                                                                                                                                                                                                                                                         Length 5234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                          1133 G;
                                                                                                                                                                                                                                                                                                                                                                         44.7%; Score 67; DB 1; Ler
llarity 100.0%; Pred. No. 1.3e-14;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 67; DB 1; Le Pred. No. 1.4e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44.7%; Scor. 100.0%; Pred. No. ... 0; Mismatches
                                                                                                                                                                                                                                                                             973 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1993.
12-MAR-1993; F00248.
13-MAR-1992; FR-003034.
(INRG) INRA INST NAT RECH AGRONOMIQUE.
Gruss A, Maguin E;
WPI; 93-303478/38.
                                                                                                                                                                                                                                                                                 1569 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q48465 standard; DNA; 6722 BP.
Q48465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67; Conservative
                                                                                                                                                                                                                                                                                 5234 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4923 GGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GGGGGCC 117
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XE AG
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                     Cereal plants containing trans-gene expressing fusion that includes signal peptide of the f12 maize gene - and protein having high content of essential amino acids, producing feeds of improved nutritional value related producing feeds of improved nutritional value.

Sclaim 14: F19 IA-H; 37pp; English.

Claim 14: F19 IA-H; 37pp; English.

This is the nuclectide sequence of a clone of the fluory2 (f12) gene of maize. It codes for a 24-kba alpha-zein protein (see W23977) that includes a 21-amino acid signal peptide (see W23976) which teargets the alpha-zein to the lumen of the rough endoplasmic reticulum. A claimed cereal plant contains a transgene comprising a first polynucleotide that encodes the f12 signal peptide and a second polynucleotide that encodes an agronomically high-value protein. Also new are seeds produced by the plants, the transgene itself, and a transgene that also includes the f12 promoter. The second polynucleotide preferably encodes a protein that has a high content of Met, Lys, Trp and/or Thr so that feeds from transformed maize, wheat, rice, barley, millet or sorghum will have increased contents of these essential amino acids in their seeds (all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                              20-JUL-1998 (first entry)
Maize fluory2 gene (fl2).
Floury2; fl2 gene; alpha-zein; signal peptide; transgenic plant; seed; essential amino acid; animal feed; maize; rice; wheat; barley; millet; sorghum; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 10529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2262 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.7%; Score 67; DB 1; Le
100.0%; Pred. No. 1.6e-14;
iive 0; Mismatches 0;
                                                                                                                                 Location/Qualifiers
1. .760
/*tag= a
//note= "vector-derived sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2484 C;
                                                                                                                                                         "vector-d.

/*tag= b

/note= "Claim 14"

3825. .4613

/*tag= c

3825.
                                                                                                                                                                                                                                                                                                                               (PION-) PIONEER HI-BRED INT INC. (UYAR-) UNIV ARIZONA STATE.

GEACH L. COLGMAN CE, LAIKINS BA; WPI; 98-110609/10.

P-PSDB; W23977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2845 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X24730 standard; DNA; 12814 BP. X24730;
                                 8/c
V09028 standard; DNA; 10529 BP.
                                                                                                                                                                                                                               /*tag= d
/88P
                                                                                                                                                                                                                                                      67; Conservative
                                                                                                                                                                                                                                                                                                22-JAN-1998.
11-JUL-1997; U11723.
17-JUL-1996; US-021833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10529 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 67; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           099 ၁၁၁၁၁၁၁ 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 GGGGGCC 117
                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                     WO9802563-A1
                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                        Zea mays.
                                                                                                                                                                                   promoter
                                                        V09028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
X24730
                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

```
9888 GIGGATCCCCCGGGCTGCAGGAATICGATATCAAGCITATCGATACCGTCGACCTCGAGG 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 GIGGAICCCCCGGGCTGCAGGAATICGAIAICAAGCTTAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; W97997, W97998.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KM(670,681)NL, was also introduced. The targetted Swedish-FAD m/hAPP gene expressed m/hAPP protein at levels approaching those
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1939 T;
21-JUN-1999 (first entry)
Swedish-FAD APP targetting vector pMTI-2398.
Amyloid precursor protein; APP; human; gene targetting; homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pMTI-2398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 44.7%; Score 67; DB 1; Length 12814; Best Local Similarity 100.0%; Pred. No. 1.7e-14; Matches 67; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-1999 (first entry)
London-FAD APP targetting vector pMTI-2453.
Amyloid precursor protein; APP; human; gene targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1962 G;
                                                                                                                                                                                                                 /standard_name= Swedish-FAD APP
/note= "encodes W97997"
5369. .6160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1850 C;
                                                                                                                                                                                                                                                                               /*tag= b
/note= "encodes W97998"
                                                                                                                                                     Location/Qualifiers
1932. .2276
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               observed for mouse APP in brain.
Sequence 12814 BP; 1865 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X24731 standard: DNA; 15692 BP. X24731;
                                                                                                  Swedish-FAD APP; mutation; ss
                                                                                                                                                                                                                                                                                                                                                         18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                     99-181029/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9948 GGGGCC 9954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 GGGGGCC 117
                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                      WO9909150-A1.
                                                                                                                                                                          mat_peptide
                                                                                                                                                                                                                                                          mat_peptide
                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                      Wirak
```

```
Jondon-FAD APP; Swedish-FAD APP; mutation; ss
                                                                Location/Qualifiers 4807, .5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2423 A;
                                                                                                                                                      replace(4849,"")
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Conservative
                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                             WO-U14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15692 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                (FARB ) BAYER CORP. Wirak DO;
                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1997; U14507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12826 GGGGGCC 12832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99-181029/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                               WO9909150-A1.
                          Homo sapiens.
                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-1997
                                                                                            mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in brain
                                                                                                                                                               mutation
                                                                                                                                                                                                                                    mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
X24733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δά
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example: Page 104-113; 209pp; English.

This is the nuclectide sequence of London-FAD APP targetting
This is the nuclectide sequence of London-FAD APP targetting
CC vector pMTI-2453. The invention provides a novel gene targetting
cc strategy that facilitates the introduction of one or more specific
mutations into any gene in a single double reciprocal homologous
cc introducing a humanised amyloid precursor protein (APP) gene into
cr cadents for producing animal models of Alzheimer's disease (AD).

CC recombination step. The method has been used particularly for
crodents for producing animal models of Alzheimer's disease (AD).

CC recombination of transgenic mice (lines ES5007, ES5103,
4 Independent lines of transgenic mice (lines ES5007, ES5103,
CC stephnique applied to embryonic stem cells. In each line, the mouse
containing a modified to encode a mouse/human hybrid (m/hAPP) where
camino acid residues 666-770 of APP770 were encoded by human cDNA
csequences instead of mouse genomic exons (exons 16-18). Within
these residues, only 3 amino acid differences exist between the
containing a humanised beta-amyloid domain. In line ES5401,
created using vector pMTI-2453, the London mutation. i.e.
CV(717), was also introduced.
Sequence 15692 BP: 2423 A; 2730 C; 2786 G; 2541 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 12766 GIGGAICCCCCGGGCIGCAGAATICGAIAICAAGCITAICGAIACGAICGACCICGAGG 12825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W97998, W97999.

Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1-UON-1999 (first entry)
Swedish/London-FAD APP targetting vector pWII-2454.
Amyloid precursor protein; APP; human; gene targetting;
Amyloid precombination; transgenic mouse; transgenic animal;
animal model; Alzheimer's disease; vector; pWII-2454;
    homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pMTI-2453; London-FAD APP; mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 67; DB 1; Length 15692;
Pred. No. 1.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                            /standard_name= "Swedish-FAD"
/note= "encodes W97999"
replace(4990,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.7%; Scor.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                 /standard_name= "London-FAD"
                                                                                                                                                                                                                                                                                                                                   /*tag= c
/note= "encodes W97998"
                                                                                                                         Location/Qualiflers
4807. .5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X24732 standard; DNA; 15692 BP. X24732;
                                                                                                                                                                                                                                                                                                            8223. .9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 100.
67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 12826 GGGGGCC 12832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 99-181029/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GGGGGCC 117
                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                              WO9909150-A1
                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S:
Matches 67;
                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wirak DO;
                                                                                                                                                                                                                                              mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAKE BAR
                NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
```

```
12766 GIGGAICCCCCGGGCIGCAGGAAITCGAIATCAAGCIIAICGAIACCGICGACCICGAGG 12825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GTGGATCCCCCGGGCTGCAGGATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 114-123; 209pp; English.

Example is page 114-123; 209pp; English.

This is the nucleotide sequence of Swedish/London-FAD APP targetting vector pWII-2454. The invention provides a novel gene targetting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous recombination step. The method has been used particularly for introducing a humanised amyloid precursor protein (APP) gene into rodents for producing animal models of Alzheimer's disease (AD).

ES5401 and ES5403 have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W97998; W98000.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into:rodents for producing models of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       App gene was modified to encode a mouse/human hybrid (m/hAPP) where amino acid residues 666-770 of APP770 were encoded by human cDNA sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 amino acid differences exist between the mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The exon-cDNA fusion gene therefore encodes an APP containing a humanised beta-amyloid domain. In line ES5103, created using vector pWII-7454, the London mutation. i.e. V7717), and the Swedish mutation, i.e. KM(670,671)NL, were introduced. The targetted Swedish/London-FAD m/hAPP gene expressed introduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        m/hAPP protein at levels approaching those observed for mouse APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2542 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.7%; Score 67; DB 1; Length 15692;
100.0%; Pred. No. 1.9e-14;
Live 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X24733 standard; DNA; 15701 BP.
x24733;
21-JUN (first entry)
swedish-FAD APP713 targetting vector pMII-2454.
Amyloid precursor protein; APP; human; gene targetting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2783 G;
                                                                                                                                                     /standard_name= "Swedish-FAD"
replace(4989,"")
                                                                                                                                                                                       replace(4989,"")
/standard_name= "London-FAD"
8223. .9023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2731 C;
/*tag= a
/note= "encodes W98000"
                                                                                                                                                                                                                                                                                                                                                 /note= "encodes W97998"
```

```
Example; Page 124-133; 209pp; English.

Example; Page 124-133; 209pp; English.

This is the nucleotide sequence of Swedish-FAD APP713 targetting vector part-255. The invention provides a novel gene targetting strategy that facilitates the introduction of one or more specific mutations into any gene in a single double reciprocal homologous crecombination step. The method has been used particularly for introducing a humanised amyloid precursor protein (APP) gene into introducing a humanised amyloid precursor protein (APP) gene into codents for producing animal models of Alzheimer's disease (AD).

C. A Independent lines of transgenic mice (lines ESS007, ESS103).

ESS401 and ESS403) have been created using the gene targetting technique applied to embryonic stem cells. In each line, the mouse technique applied to embryonic stem cells. In each line, the mouse amino acid residues 666-770 of APP770 were encoded by human cDNA sequences instead of mouse genomic exons (exons 16-18). Within these residues, only 3 amino acid differences exist between the mouse and human proteins, i.e. Gly-676 to Arg, Phe-681 to Thr and Arg-684 to His. The exon-DNA fusion gene therefore encodes an APP created using vector pMTI-2455, the Swedish mutation. i.e.

EXM(670,681)ML, was also introduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 99-181029/15.
P-PSDB; W97998, W98001.
Modification of target nucleic acids - by homologous recombination, used particularly for introducing a humanised amyloid precursor protein gene into rodents for producing models of Alzheimer's
homologous recombination; transgenic mouse; transgenic animal; animal model; Alzheimer's disease; vector; pWTI-2455; Swedtsh-FAD APP713; mutation; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2845 G;
                                                                                                                                                                                        /*tag= b
/standard_name= "Swedish-FAD"
replace(4981,"")
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2675 C;
                                                                                                                                                                                                                                                           /standard_name= APP713stop
8232. .9032
/*tag= d
/note= "encodes W97998"
                                                                                             Location/Qualifiers
4807. .4983
/*tag= a
/note= "encodes W98001"
                                                                                                                                                                      replace(4835,"")
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2470 A;
                                                                                                                                                                                                                                                                                                                                                          25-FEB-1999.
18-AUG-1997; U14507.
18-AUG-1997; WO-U14507.
                                                                                                                                                                                                                                                                                                                                                                                                               (FARB ) BAYER CORP.
                                                                                                                                                                                                                                                                                                                                       WO9909150-A1.
                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                      Wirak DO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seguence
                                                                                                                                                                      mutation
                                                                                                                                                                                                                            mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease
```

Qy 51 GTGGATCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
Db 12775 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 12834

ô

Gaps '

ô

Query Match 44.7%; Score 67; DB 1; Length 15701; Best Local Similarity 100.0%; Pred. No. 1.9e-14; Matches 67; Conservative 0; Mismatches 0; Indels

111 GGGGGCC 117

ò

Db 12835 GGGGCC 12841

Search completed: May 29, 2000, 21:58:40 Job time: 38188 sec

-	* **.				
er i				•	
A. F					
4				o <b>ie</b> ¹	7
#.					
A.					
# #					
\$					
	•			1.0	
* 8.					
	*	:		4	
	War in the second of the secon				and the second
					1.2
			The second secon		r d
				in the state of	
d.					
	A STATE OF THE STA			i j	
<b>.</b> .					
	The second of th				3
	And the second of the second o				. 생
Ĺ					*
				Χ.	1
2.					2.4
					· · · · · · · · · · · · · · · · · · ·
	34.				
					4
					. 4
A		the control of the co			
N Bar	4 · ·				
			K.		
;				1. 12. 12. 13. 13. 13. 13. 13. 13. 13. 13. 13. 13	
; p:					
100					1
È				<b>e</b>	
					4
					1
			No.		
				•	
		\$ 4	A Section of the Control of the Cont	•	
					1
			•		
	: 2		en e		
				#	
				- 1941 - A	
			y Articles		. 7.
4					
			<b>a</b> '		
				4	
			*.		* · ·
	*	and the second of the second o		4 - 34	gar Agrica
	en e				
<b>&gt;</b>					Production of the second
1					1.
	<b>**</b>				P. 1
	· · · · · · · · · · · · · · · · · · ·			7	· · · · · · · · · · · · · · · · · · ·
				and the second	i j
	A.				•
1 to 1				9 W	<b>.</b>
IR.				Mark Mark	

Page 1

```
Query Match
Best Local Similarity
Matches 80; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-08-967-101-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02110
0000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 121, App
Sequence 121, App
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 113, App
Sequence 113, App
Sequence 62, Appl
Sequence 18, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1, Appli
2, Appli
2, Appli
3, Appli
3, Appli
6, Appli
6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56, Appl
1, Appl
1, Appli
1, Appli
1, Appli
2, Appli
1, Appli
1, Appli
                                                                                                              May 29, 2000, 22:09:10 ; Search time 621.83 Seconds (without alignments) 31.355 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Al Sequence 2, Al Sequence 3, Al Sequence 3, Al Sequence 5, Al Sequence 11, Al Sequence 11, Al Sequence 11, Al Sequence 11, Al Sequence 2, Al Sequence 3, Al Se
                                                                                                                                                                                                 150
1 GGCCAAAAATTGAAAAACTA......TTGTTTTTTGTGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, A Sequence 1, A Sequence 10, Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, 8
Sequence 2, 8
Sequence 2, 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgnl_6/ptodata/1/ina/5A_COMB.seg:*
/cgnl_6/ptodata/1/ina/5B_COMB.seg:*
/cgnl_6/ptodata/1/ina/5C_COMB.seg:*
/cgnl_6/ptodata/1/ina/5C_COMB.seg:*
/cgnl_6/ptodata/1/ina/R_COMB.seg:*
/cgnl_6/ptodata/1/ina/PCTUS_COMB.seg:*
/cgnl_6/ptodata/1/ina/PCTUS_COMB.seg:*
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-967-101-121
US-08-952-541-121
US-08-302-752-1
US-08-302-752-1
US-08-302-752-1
US-08-302-752-3
US-08-302-752-3
US-08-992-334-3
US-08-992-334-3
US-08-992-334-3
US-08-793-610-6
US-08-793-610-6
US-08-793-610-6
US-08-465-315-56
US-08-465-315-56
US-08-866-754-1
US-08-967-10-1
US-08-967-10-1
US-08-967-10-1
US-08-967-101-113
US-08-967-101-113
US-08-967-101-113
US-08-967-101-113
                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                             230463 seqs, 64992525 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
                                                                                                                                                                                                                                             IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_NA:*
                                                                                                                                                                                US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.2
62.4
62.4
59
                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                 OM nucleic
                                                                                                                                                                                                                 sednence:
                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database
                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                  Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           υ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0000000
```

```
ö
                                                           Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                               Appli
Appli
Appli
Appli
Appli
Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                        Sequence 3, Sequence 3, Sequence 3, Sequence 3, Sequence 15, Sequence 16, Sequence 17, Sequence 1, Sequence 2, Sequence 3, Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 121, Application US/08967101
Fatent No. 584054c
GENERAL INFORMATION:
APPLICANT: ST GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: GALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURMITZ & THIBEAULT
STREET: HIGH Street TOWER - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.5%; Score 69.8; DB 3; Length 793; larity 82.5%; Pred. No. 4.5e-16; Conservative 0; Mismatches 17; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PCIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
US-08-967-101-116
US-08-957-101-116
US-08-011-398B-3
US-08-011-398B-3
US-08-662-498-3
US-08-667-426-15
US-08-076-726-15
US-08-076-726-15
US-08-897-719-8
US-08-897-719-8
US-08-465-918-1
US-08-465-918-1
US-08-6680-395-4
US-08-680-395-4
US-08-680-395-4
US-08-680-395-4
US-08-680-395-4
US-08-663-267-3
US-08-663-267-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPLICATION NOTE PILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: PITCHE Edwund R.
TELECHONE: (617) 248-7100
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121: SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
US-08-967-101-121
     STATE: Massachusetts
COUNTRY: U.S.A.
```

```
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christie Parker & Hale, LLP
STREET: 350 West Colorado Boulevard, Suite 500
CITY: Pasadena
STATE: California
COUNTRY: United States
ZIP: 91105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular MOLECULE TYPE: DNA (9e HYPOTHETICAL: NO ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
CLONE: pG+host4
US-08-992-334-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3481 GGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-302-752-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 GGAGGCCGCGGGGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACG 71
            39 GGCGCCATGACGTGGATCCCCGGGCTGCAGAATTCGATATCAAGCTTATCGATACCG 98
                                  130 GGAGGCGGGGGGGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.08-992-334-1/c

| Sequence 1, Application US/08992334
| Patent No. 5919616
| GENERAL INFORMATION:
| APPLICANT: Gruss, Alexandra | APPLICANT: Maguin, Emmanuelle | TITLE OF INVENTION: METHODS FOR USING A TEMPERATURE-SENSITIVE | TITLE OF INVENTION: PLASMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                          NESOUR 5.20-541-121/c

Sequence 121, Application US/08592541

SEQUENCE 181

APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: FRASER, PAUL E

TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED

TITLE OF INVENTION: TO ALZHEIMER'S DISEASE

NUMBER OF SEQUENCES: 183

CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; DB 4; Length 793;
4.5e-16;
thes 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARENTE Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 TCGACCICGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 TCGACCTCGAGGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                         46.5%; Score 69.8; DE
82.5%; Pred. No. 4.5e-
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7000
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 82.5%
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-592-541-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                     g
                                                                                                                ò
                                                                                                                                                       g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 44.7%; Score 67; DB 4; Length 3792; Best Local Similarity 100.0%; Pred. No. 7.9e-15; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: THERMOSENSIBLE PLASMID NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM: MEDIUM TYPE: Flopy disk COMPUTER: IBM PC compatible OMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION NUMBER: US/08/302,752
APPLICATION NUMBER: US/08/302,752
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PF FF 92/03034
FILING DATE: 13-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: PFOUL, D. BIUGE
REGISTRATION NUMBER: C93:31779
TELECHONE: (626) 795-9900
TELECHONE: (626) 795-9900
INFORMATION FOR SEQ ID NO: 1:
CROSSIFICATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08302752; Patent No. 6025100
GENERAL INFORMATION:
```

```
VESOLI

VESOLI

Sequence 2, Application US/08992334

Sequence 2, Application US/08992334

Patent No. 5919678

SEQUENCE 1 NFORMATION:

APPLICANT: Maguin, Emmanuelle

TITLE OF INVENTION: PLASMID

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christie Parker 6 Hale, LLP

STREET: 350 West Colorado Boulevard, Suite 500

CITY: Pasadena

STATE: California

COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 3031..3765
FEATURE:
NAME/KEY: - 31434
LOCATION: 1433..1434
                                                                                                                                                       exon
1620..1733
                                                                                                                                                                                                                   exon
2047..2174
                                                                                                                                                                                                                                                                                              2267..2425
                                                                                                                                                                                                                                                                                                                                        exon
2567..2751
                                                                                                                                                                                                                                                                                                                                                                                                    exon
2828..2921
                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3999 GGGGGCC 4005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                            NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                     NAME/KEY:
LOCATION:
                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                           LOCATION:
FEATURE:
                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08410540
Petent No. 5807678
GENERAL INFORMATION:
APPLICANT: Miller, Walter L.
APPLICANT: Lin, Dong
APPLICANT: Strauss III, Jerome F.
TITLE OF INVENTION: IDENTIFICATION OF GENE MUTATIONS
TITLE OF INVENTION: ASSOCIATED WITH CONGENITAL LIPOID ADRENAL HYPERPLASIA NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                              Query Match

44.7%; Score 67; DB 5; Length 3792;
Best Local Similarity 100.0%; Pred. No. 7.9e-15;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,540
FILING DATE: 23-MAR-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFISTRATION NUMBER: 30,092
REFISTRATION NUMBER: UCAL-238/00US
TELECOMMUNICATION INFORMATION:
TELEFAX: 415 853 5070
TELEFAX: 380816COOLEYPA
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4016 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FF/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3792 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: single
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) US-08-302-752-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 5 Palo A CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3481 GGGGGCC 3475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΩS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 5
US-08-410-540-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
```

```
OTHER INFORMATION: /note= "interruption of sequence data" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: -
LOCATION: 2208..2209
OTHER INFORMATION: /note= "interruption of sequence data"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
LOCATION: 2781..2782
OTHER INFORMATION: /note- "interruption of sequence data"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: 2956..2957
; OTHER INFORMATION: /note= "interruption of sequence data"
US-08-410-540-3
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEX: exon
LOCATION: 1098 1222
```

51 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110 0; Gaps Query Match
44.7%; Score 67; DB 2; Length 4016;
Best Local Similarity 100.0%; Pred. No. 8e-15;
Matches 67; Conservative 0; Mismatches 0; Indels

ö

3939 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 3998

Gaps

```
4983 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 4924
                                                                                                                                                                                                                                                                                                                                            51 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
44.7%; Score 67; DB 5; Length 5234;
Best Local Similarity 100.0%; Pred. No. 8.8e-15;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: PALDS
COMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: Patentin Elease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 08/302,752
FILING DATE: 24-DEC-1994
FILING DATE: 12-MER: 1993
PRICATION NUMBER: PCT/FR93/00248
FILING DATE: 12-MER: 1993
PRICATION NUMBER: PCT/FR93/00248
FILING DATE: 13-MER: 1993
ATTORNEY/AGENT INFORMATION:
NAME: PROUK DATA:
RESISTRATION NUMBER: C9958
REFERENCE/COCKET NUMBER: C99:1779
FILING DATE: 13-MER: C99:1779
FILING DATE: 13-MER: PR FR92/03034
FILING DATE: 13-MER: C99:88
REFERENCE/COCKET NUMBER: C99:31779
TELECOMMULCATION INFORMATION:
MELEPRONE: (626) 795-9900
                   LENGTH: 5234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-302-752-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: DNA (genomic) US-08-992-334-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (626) 577-8800 INFORMATION FOR SEQ ID NO: 3 SEQUENCE CHARACTERISTICS: LENGTH: 6722 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: California
COUNTRY: United States
ZIP: 91105
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4923 GGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4983 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 4924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 44.7%; Score 67; DB 4; Length 5234; Best Local Similarity 100.0%; Pred. No. 8.8e-15; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08302752

Sequence 2, Application US/08302752

Patent No. 6025190

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
                                                                                                                      CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/992,334
FILING DATE: 17-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/302,752
FILING DATE: 24-DEC-1994
PRIOR APPLICATION NUMBER: ETFR92/03034
PRIOR APPLICATION NUMBER: ETFR92/03034
FILING DATE: 12-WAR-1993
PRIOR APPLICATION NUMBER: CS-050334
FILING APPLICATION NUMBER: CS-050334
FILING APPLICATION NUMBER: CS-050334
FILING PAPLICATION NUMBER: CS-050334
FILING PATON NUMBER: CS-050334
FILING CATON NUMBER: CS-050334
FILING NUMBER: CS-050334
FILING NUMBER: CS-050334
FILING SATION NUMBER: CS-050331779
TELECOMMUNICATION NO: 2:
SEQUENCE CHRARACTERISTICS:
LENGTH: S-234 base Patirs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILLING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO FR/93/00248
FILLING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 2:
ZIP: 91105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
US-08-992-334-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4923 GGGGGCC 4917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-302-752-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
```

g

ò

g

ö

```
5650 TAATGGGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTC 5709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 TGACGIGGATCCCCCGGGCTGCAGGAATICGATATCAAGCTTAICGATACCGTCGACCTC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 44.1%; Score 66.2; DB 3; Length 9318; Best Local Similarity 95.8%; Pred. No. 2.1e-14; Matches 68; Conservative 0; Mismatches 3; Indels 0.
                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 56, Application US/08463115
Patent No. 5703221
GENERAL INFORMATION:
APPLICANT: WILLIAM JOHN MARTIN
TITLE OF INVENTION: AND RELATED VACCINES
INTILE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSED: Lyon & Lyon
STREET: Sai west Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: Galifornia
COMPTRY: U.S.A.
COMPTRY: U.S.A.
MEDIUM TYPE: Storage
MEDIUM TYPE: Storage
655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION NUMBER: DE P 44 31 973.8
APPLICATION NUMBER: DE P 44 31 973.8
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INPORMATION:
NAME: BETMEN, RICHARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REFERNEL/POCKET NUMBER: P1614-7007
TELECOMMUNICATION:
TELEPHONE: (202)638-5000
                                                              COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: DNA US-08-793-610-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5710 GAGGGGGGCC 5720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 GAGGGGGGCC 117
                        Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-463-115-56
                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                   ö
                                                                                                                                      6471 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 6412
                                                                                                              51 GIGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08793610
Patent No. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, CHIStopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEROF
INDER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                   ö
                   Length 6722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 6722;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 44.7%; Score 67; DB 5; Length 672; Best Local Similarity 100.0%; Pred. No. 9.6e-15; Matches 67; Conservative 0; Mismatches 0; Indels
                   Query Match 44.7%; Score 67; DB 4; Length 672
Best Local Similarity 100.0%; Pred. No. 9.6e-15;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nikaido, Marmelstein, Murray & Oram LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
IITLE OF INVENTION: THERMOSENSIBLE PLASMID
NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO FR/93/00248
FILING DATE: 12-MAR-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 6722 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9203034
FILLING DATE: 13-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08302752 Patent No. 6025190 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: DNA (genomic) US-08-302-752-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6411 GGGGGCC 6405
                                                                                                                                                                                                                                                     6411 GGGGGCC 6405
                                                                                                                                                                                                       111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                         US-08-302-752-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-793-610-6
```

g ò

ô

```
51 GIGGAICCCCCGGGCIGCAGGAAITCGAIAICAAGCIIATCGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
US-00-204-675-1
Squence 1, Application US/08204675
Squence 1, Application US/08204675
Squence 1, Application US/08204675
Squence 1, Application US/08204675
SAPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jef D.
TITLE OF INVENTION: In Vitro Transposition of Artificial ITLE OF INVENTION: IT Application of Artificial ITLE OF INVENTION: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
41.6%; Score 62.4; DB 2; Length 685;
Best Local Similarity 94.0%; Pred. No. 1.9e-13;
Matches 63; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                  Four
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: TEM PC comparatible
COMPUTER: Patentin Rolease #1.0, Version #1.25
SOFTWARE: Patentin Rolease #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION UNBER: US/08/204,675
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
                                                           ; OTHER INFORMATION:
US-08-465-388-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 GGGGGNC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.6%; Score 62.4; DB 2; Length 685;
Best Local Similarity 94.0%; Pred. No. 1.9e-13;
Matches 63; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                           Four
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,115
FILING DATE: Une 5, 1995
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA: including application prior APPLICATION DATA: including application PRIOR APPLICATION DATA: including application PRIOR APPLICATION DATA: described below: APPLICATION NUMBER: 08/15,811
FILING DATE: May 22, 1992
APPLICATION NUMBER: 07/704,814
FILING DATE: May 22, 1991
APPLICATION NUMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 07/704,814
FILING DATE: SEPTEMBER: 07/704,814
FILING DATE: May 23, 1991
APPLICATION NUMBER: 20, 1991
ATTORNEY NUMBER: 213/301
TELEFRAX: (213) 489-1600
TELEFAX: (7-3310
INFORMATION FOR SED ID NO: 56: SEQUENCE CHARACTERISTICS:
LENGTH: 685 DASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: SINGIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 56, Application US/08465388

Patent No. 5753488
GENERAL INFORMATION:
GRERRAL INFORMATION:
TITLE OF INVENTION: ISOLATED STEALTH VIRUSES
TITLE OF INVENTION: AND RELATED VACCINES
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
SOFTWARE: FASTSEQ VETSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
US-08-463-115-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 GGGGGNC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-08-465-388-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           පු
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ద
```

```
2044 GIGGAICCCCCGGGCTGCAGAAIICGAIATCAAGCIIAICGAIACCGICGACCTCGAG 2102
                                                                                                                                                                                                                                                                                                     51 GIGGAICCCCCGGGCIGCAGGAAITCGAIATCAAGCITAICGAIACCGICGACCICGAG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Boeke, Jef D.
APPLICANT: Boeke, Jef D.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: Banner, Birch, McKie, and Beckett
STREET: 1010 Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 4164; 6e-12;
                                                                                                                                                                                                                  39.3%; Score 59; DB 3; Length 4164; 100.0%; Pred. No. 6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,364
                                                                                                                                                                                                                                         Best Local Similarity 100.0%; Pred. No. 6e-
Matches 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DALE.

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.4550:
TELECOMMUNICATION INFORMATION:
TELEFAK: 202.508,999
TELEX: 197430 BBMB UT
TELEFAK: 202.508,999
TELEX: 197430 BBMB UT
SEQUENCE CHARATERISTICS:
LENGTH: 4164 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPPLOGY: circular
MOLECULE TYPE: DNA (Genomic)
""""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39.3%; Score 59; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,141
ER: 01107.45501
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08796364
Patent No. 5968785
                        TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: PAT-1
US-08-660-754-1
      double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
IMMEDIATE SOURCE:
      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; CLONE: PAT-1
US-08-796-364-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20001
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
US-08-796-364-1
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Devine, Scott E.
APPLICANT: Boeke, Jef D.
APPLICANT: Braitermen, Lelita T.
TITLE OF INVENTION: In Vitro Transposition of Artificial
TITLE OF INVENTION: Transposons
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKle, and Beckett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.3%; Score 59; DB 1; Length 416d Best Local Similarity 100.0%; Pred. No. 6e-12; Matches 59; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/204,675
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.45501
TELECHONE: 202.508.9100
ATTORNEY/AGENT INFORMATION:

NAME: REGISTRATION NUMBER: 32,141

REGISTRATION NUMBER: 01107.45501

TELECOMMUNICATION INFORMATION:
TELEFAX: 202.508.9109

TELEFAX: 202.508.929

TELET: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4164 base pairs
TYPE: nucleic acid
STRANDEDNESS: 00uble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08660754
Patent No. 5843772
                                                                                                                                                                                                                                                                            TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202.508.9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4164 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                  US-08-204-675-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-660-754-1
```

a ò

; 0 0; Gaps 0; Indels 0; Mismatches Matches 59; Conservative

Search completed: May 29, 2000, 22:09:16 Job time: 38757 sec

Run on:

```
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                               Cgnl_6/ptodata/1/pna/US092D_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US092D_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US093B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US093B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US093B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US093B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US093B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US094B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US094B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US094B_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US000A_COMB.Seq:*

Cgnl_6/ptodata/1/pna/US001A_COMB.Seq:*

Cgnl_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgnl_6/ptodata/1/pna/USO7_NEW_COMB.seq:
/cgnl_6/ptodata/1/pna/USO8_NEW_COMB.seq:
/cgnl_6/ptodata/1/pna/USO9_NEW_COMB.seq:
/cgnl_6/ptodata/1/pna/US60_NEW_COMB.seq:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn1_6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0
92.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
S
                                                                                                                                                                                May 30, 2000, 09:48:32 ; Search time 2276.24 Seconds (without alignments) 294.022 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                         150
1 GGCCAAAAATTGAAAAACTA......TTGTTTTTGTGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10285240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pending_Patents_NA:*

1: /cgnl_6/ptodata/1/pna/USO6_COMB.seq:*
2: /cgnl_6/ptodata/1/pna/USO6_COMB.seq:*
3: /cgnl_6/ptodata/1/pna/USO8_COMB.seq:*
4: /cgnl_6/ptodata/1/pna/USO80_COMB.seq:*
5: /cgnl_6/ptodata/1/pna/USO81a_COMB.seq:*
6: /cgnl_6/ptodata/1/pna/USO81a_COMB.seq:*
7: /cgnl_6/ptodata/1/pna/USO81a_COMB.seq:*
8: /cgnl_6/ptodata/1/pna/USO81a_COMB.seq:*
9: /cgnl_6/ptodata/1/pna/USO82a_COMB.seq:*
10: /cgnl_6/ptodata/1/pna/USO82a_COMB.seq:*
11: /cgnl_6/ptodata/1/pna/USO82a_COMB.seq:*
12: /cgnl_6/ptodata/1/pna/USO82a_COMB.seq:*
13: /cgnl_6/ptodata/1/pna/USO83a_COMB.seq:*
14: /cgnl_6/ptodata/1/pna/USO83a_COMB.seq:*
14: /cgnl_6/ptodata/1/pna/USO83a_COMB.seq:*
15: /cgnl_6/ptodata/1/pna/USO83a_COMB.seq:*
16: /cgnl_6/ptodata/1/pna/USO84a_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgnl_6/ptodata/1/pna/US085_COMB.seq:
/cgnl_6/ptodata/1/pna/US085_COMB.seq:*
/cgnl_6/ptodata/1/pna/US087a_COMB.seq:*
/cgnl_6/ptodata/1/pna/US087c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US087c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US088c_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089c_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089E_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089C_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
/cgnl_6/ptodata/1/pna/US089L_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'ptodata/1/pna/US090B_COMB.seq
'ptodata/1/pna/US090C_COMB.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn1_6/ptodata/1/pna/US091C_COMB.seq
/cgn1_6/ptodata/1/pna/US092A_COMB.seg
                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5142629 seqs, 2230885800 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                   OM nucleic
                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
```

Database

Sequence 9, Appli Sequence 8, Appli

US-08-935-377-9 US-08-935-377-8

28 28

150

П

SUMMARIES

Description

/ptodata/1/pna/US6017C_COMB.seq:*/ptodata/1/pna/US6018A_COMB.seq:*/ptodata/1/pna/US6018B_COMB.seq:* /ptodata/1/pna/US6018C_COMB.seq:* 'ptodata/1/pna/US6019_COMB.seq

us-08-935-377-9.rnp

```
Gaps
                                                                                                                                                                                                                                                                                                                               1 GGCCAAAAAITGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGACGTGGATCCCC 60
                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08935377

Sequence 8, Application US/08935377

Sequence 8, Application:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600

STATE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                   Length 150;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
SEGTWARE: PatentIn Release #1.0, Version #1.30
SOUTHARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
FILING DATE: 22-SEP-1997
FILING DATE: 23-SEP-1997
ATTORNEY AGENT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 1821.001000/EKS/CMB
TELEPHONE: (202) 371-260
TELEPHONE: (202) 371-240
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NAME: Steffe, Eric K
REGISTANTION NUMBER: 36,688
REFERENCE-PLOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 150 base pairs
TYPE: nucleic acid
STRANDENNESS: SINGle
                                                                                                                                                                                                                                                               Query Match
100.0%; Score 150; DB 28;
Best Local Similarity 100.0%; Pred. No. 9.3e-42;
Matches 150; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear;
MOLECULE TYPE: CDNA
US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:
US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-08-935-377-8
                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                       Sequence 27, Appli
Sequence 31, Appl
Sequence 595, App
Sequence 8570, Ap
Sequence 8570, Ap
Sequence 8523, Ap
Sequence 8523, Ap
Sequence 8595, Ap
Sequence 8595, Ap
Sequence 3939, Ap
Sequence 2939, Ap
Sequence 2334, Ap
Sequence 2334, Ap
Sequence 2495, Ap
Sequence 2255, Ap
Sequence 2255, Ap
Sequence 2255, Ap
                                                                                                                                                                        , Appli
1, Appli
1, Appl
95, App
                                                                                                                                            Sequence 12
                                                                             Sequence 12
Sequence 12
Sequence 12
                                                                                                                             Sequence 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Squence 9, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Mashington
STATE: D. C.
COUWRRY: USA
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 2
Sequence 2
Sequence 1
Sequence 1
Sequence 9
Sequence 9
Sequence 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence (
                                                                                                                                                            Sequence ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
          US-08-935-377-6
US-08-935-377-6
US-08-436-491-121
US-08-496-841-121
US-08-509-359-121
US-08-509-359-121
US-09-124-523-121
US-09-124-523-121
US-09-124-523-121
US-09-124-523-121
US-09-124-523-121
US-09-127-480-121
US-09-127-480-121
US-09-127-480-121
US-09-312-782-8570
US-09-312-694-8595
US-09-312-694-8595
US-09-312-694-8595
US-09-313-782-8595
US-09-313-782-8595
US-09-313-473-2360
US-09-313-473-2100
US-09-328-351-2255
US-09-328-351-2360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 1
US-08-935-377-9
               136
136
130
69.8
69.8
69.8
69.8
                                                                                                                                                                                              67.8
```

g ô a ò g

ò

```
61 CGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGCCAAAAATIGAAAAACTAGAICTATITATIGCACGCGGCCGC----CGIGGAICCCC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGACGTGGATCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Sulte 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-08-431-048A-121/C
Sequence 121, Application US/08431048A
SEQUENCE 121, Application US/08431048A
SEQUENCE INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMENS, PAUL E
ITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
ITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTE: 20009

COMPUTE: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,377
FILING DATE: 22-SEP-1997
CLEASIFICATION: 424
ATTORNEY/AGBNT INFORMATION:
NAME: Steffe, Eric K
REGISTRATION NUMBER: 36.68
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUTCATION INFORMATION:
TELEPHONE: (202) 311-260
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Patent Administrator, TESTA, HURWITZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 130; DB 28;
Pred. No. 7.5e-35;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 CTAACTAATTTTGTTTTGTGGGCCCGGCC 150
119 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 CTAACTAATTTTGTTGTGGGCCCGGCC 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.7%;
Matches 145; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                               CITY: Washington
STATE: D. C.
COUNTRY: USA
                                                                  RESULT 4
US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-935-377-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ä
                                                                                                                                                                                                  CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCTAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 CGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACGCGGGGGGGCCTAA 118
                                                                                                                                                                                                                                               1 GGCCAAAAATTGAAAACTAGATCTATTTATTGCACGCGGCCGCCATG--GTGGATCCCC 58.
                                                                  Gaps
                                                                                                                                  1 GGCCAAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGACGTGGATCCCC 60
                                                                                                            1 GGCCAAAAATTGAAAAACTAGAICTATTTATTGCACGCGGCCGCCAIGACGTGGATCCCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/08935377
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
TITLE OF INVENTION: T Cells Specific for Target Antigens and
TITLE OF INVENTION: Vaccines Based Thereon
NUMBER OF SEQUENCES: 37
CORRESPONDENCES Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, N.W., Suite 600
                       Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OOFERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PSPLICATION NUMBER: US/08/935,377 FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
              Score 138; DB 28;
Pred. No. 1.3e-37;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Steffe, Etlc K
REGISTRATION NUBER: 36,688
REFERENCE/DOCKET NUMBER: 1821.0010000/EKS/CMB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ 1D NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 136; DB 28;
Pred. No. 6.4e-37;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                            121 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                 120 CTAACTAATTTTGTTTTTGTGGGCCCGGCC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAACTAATTTTGTTTTTGTGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.78;
                  92.0%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 98.73
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 148 base pairs
                                                                  Matches 149; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D. C.
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-935-377-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
```

ï

8 5; Gaps

셤

ò

g

ö

à

```
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 écasecceseccesariccecesecrecaseaarrecararerasecraraces 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 793;
                                                                                                                                                                                                                                                                                                                                                                Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 121, Application US/08509359
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: FRASE, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusels
COUTRY: U.S.A.
COUTRY: U.S.A.
ZIP: 0.2110
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATION
COMPUTER: IBM PC COMPATION
FILING DATE: 31-JUL-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
MARNE: TWOMMEY, Michael J
REGISTRATION NUMBER: 38349
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46.5%; Score 69.8; DB 17;
ilarity 82.5%; Pred. No. 7.9e-14;
Conservative 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                             Score 69.8; DB 16;
Pred. No. 7.9e-14;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Testa, Hurwitz & Thibeault
High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 38349
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7362
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-496-841-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 12 SEQUENCE CHARACTERISTICS: LENGTH: 793 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                Query Match

Best Local Similarity 82.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 80; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Tes
STREET: High S
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-509-359-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 GGAGGCCGCGGGGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 82.5%; Pred. No. 7.9e-14;
Matches 80; Conservative 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121, Application US/08496841
Sequence 121, Application US/08496841
Sequence 121, Application
APPLICANT: St. George-Hyslop, Peter
APPLICANT: Rommens, Johanna M.
APPLICANT: Fraser, Paul E.
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibeault
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                            COMPUTER REALBABLE FURNE

COMPUTER: IBM PC COMPAtible

COMPUTER: IBM PC COMPATIBLE OF US/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/431,048A

FILING DATE: 28-APR-1995

CLASSIFICATION: 800

ATTOMNEY/AGENT INPORMATION:

NAME: TWOMPY, MIChael J

REGISTRATION NUMBER: 38,349

REGISTRATION NUMBER: 38,349

REGISTRATION INFORMATION:

TELEPHONE: (617) 248-7000

TELEFRAM: (617) 248-7000

TELEFRAM: (617) 248-7100

TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 TCGACCTCGAGGGGGGCCCGGTACCCAGCTTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/496,841
FILING DATE: 28-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) US-08-431-048A-121
                   ADDRESSEE: THIBEAULT, LLP
STREET: 125 High Street
CITX: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREEL.
CITY: Boston
STATE: Massachusetts
                                                                                                                                          ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-496-841-121/c
```

g ò Gaps

1

```
ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
39 GCCCGCCATGACGTGCATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 GGAGGCCGGGGCGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 69.8; DB 17; Length 793; Pred. No. 7.9e-14; 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                              US-08-509-359B-121/C
Sequence 121, Application US/08509359B
Sequence 121, Application US/08509359B
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 121, Application US/09124523
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: ROMMENS, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: LERNER, DAVID, LITTENBERG, KRUMHOLZ & MENTLIK
600 South Avenue West
                                                                                              99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                        10 TCGACCTCGAGGGGGCCCGGTACCCAGCTTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CINTY: Westilled

COUNTRY: U.S.A.

ZINE: 0709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word, Version 6.0c
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 02/08/509,359B
FILING DATE: 31-UL-95
CLASSIFICATION: NUMBER: 3629
FILING DATE: 71-UL-95
CLASSIFICATION: NUMBER: 3629
TELECOMMUNICATION INFORMATION:
TELEPRAX: (908) 654-5000
TELEPRAX: (908) 654-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 82.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Westfield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-124-523-121/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
STREET: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-509-359B-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                g
                                                                                              ò
                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        쉽
       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121, Application US/09124698
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMENS, JOHANNA M
APPLICANT: RASSER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 46.5%; Score 69.8; DB 40; Length Best Local Similarity 82.5%; Pred. No. 7.9e-14; Matches 80; Conservative 0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/124,523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                      ADDRESSEE: TESTA, HURWITZ & THIBEAULT STREET: High Street Tower - 125 High Street CITY: Boston: ASTATE: MASSACHUSELTS COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATONNE/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELEPHONE: (617) 248-7100
TELEPHONE: (617) 248-7100
TELEPHONE: CAPACTERISTICS:
EDWOTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOMBERNESS: SINGLE
TOMBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/124,69E
                                                                                                                                                                                                                                                                                                                 COMPUTER READAELE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-124-523-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-124-698-121/c
                                                                                                                                                                                                                                                                      02110
```

ô

```
51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                     39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: HOSOI, Shigeru, FUKAMI, Tadashi, HIYOSHI, Makiko TITLE OF INVENTION: Method of Determining Base Sequence of TITLE OF INVENTION: Nucleic Acid NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSE: Cushman Darby 6 Cushman STREET: Ninth Floor, 1100 New York Avenue, N.W. CITY: Washington
                                                Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 69; DB 13; Length 224;
Pred. No. 1e-13;
0; Mismatches 10; Indels
                                                                                             Indels
                                                Score 69.8; DB 40;
Pred. No. 7.9e-14;
0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett, 3.5 inch, 720Kb storage OPERATING SYSTEM: MS-DOS SOFFWARE: WordPerfect 5.1 or ASCII editors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Other nucleic acid Synthetic DNA
                                                                                                                                                                                                                        99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                    FILING DAIE: 2. CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: JP691/1994
FILING DATE: 26-JNN-1994
FILING DATE: 26-JNN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Glenn J. Perry
REGISTRATION NUMBER: 28458
TELECHMUNICATION INFORMATION:
TELEPHONE: (202)861-3000
TELEFAX: (202)862-0944
TELEFIX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACIERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/377,383
FILING DATE: 25-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GGGGCCTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGGCCCGGTACCCAGCTTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08377383
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 88.2%;
Matches 75; Conservative
                                                    Query Match
Best Local Similarity 82.5%;
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
JS-09-127-480-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-377-383-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                               g
                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GGCCGCCATGACGTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                      Length 793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESSS:
CORRESPONDENCE ADDRESSS:
CARRESPONDENCE TOWERS:
STREET: High street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

46.5%; Score 69.8; DB 40;
Best Local Similarity 82.5%; Pred. No. 7.9e-14;
Matches 80; Conservative 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 TCGACCTCGAGGGGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 rcgaccrcgaggggggggccggracccagcrrrgrr 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 121, Application US/09127480
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: PITCHET, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7100
TELEFAX: (617) 248-7100
INFORMATION FOR ESQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDENESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 121:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear;
; MOLECULE TYPE: DNA (genomic)
US-09-124-698-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
```

```
5 AAAAATTGAAAAACTAGATCTATTTATTGCACGCGGCCGCCATGACGTGGATCCCCCGGG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65 CTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.7%; Pred. No. 4.4e-13;
Matches 84; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TREE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SUSTRANT APPLICATION DATA:
APPLICATION NUMBER: US/60/061,998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
Sequence 31, Application US/09072433
SEQUENCE 31, Application US/09072433
SEQUENCE 31, Application US/09072433
SEREMAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: BIOREMEDIATION
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABJE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,433
FILING DATE: 04-MAY-1998
CLASSIFICATION: 514
                      CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.STREET: 3174 PALO ALTO
STREET: PALO ALTO
STATE: CALIFORNIA
COUNTX: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PM-0006-2P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE (650) 855-0555
TELECAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-60-061-998-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                       Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCES OF STREPTOCOCCUS PNEUMONIAE GENOME, FRAGMENTS THEREOF, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 GIGGAICCCCCGGGCIGCAGGAATICGAIAICAAGCITAICGAIACCGICGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08693573
GENERAL INFORMATION:
APPLICANT: HOSOI, Shigeru,
APPLICANT: FUKAMI Tadashi,
APPLICANT: KOJIMA, Makiko
TITLE OF INVENTION: Method of Determining Base Sequence of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: USHMAN DARBY CUSHMAN
ADDRESSEE: INTELLECTUAL PROPERTY GROUP OF
ADDRESSEE: PILLSBURY MADISON & SUTRO, L.L.P.
STREET: Washington
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

46.0%; Score 69; DB 18; Length 224;
Best Local Similarity 88.2%; Pred. No. 1e-13;
Matches 75; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

ZIP: 20005-3918

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 720Kb storage COMPUTER: TEBM PC/XT/AT compatibles
COMPUTER: DISKETTE, MS-DOS
COMPUTER: WordPerfect 5.1 or ASCII editors
COMPUTER: WordPerfect 5.1 or ASCII editors
SOFTWARE: WordPerfect 5.1 or ASCII editors
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,573
FILING DATE: 07-AUG-1995
CLASSIFICATION ADATA:
APPLICATION NUMBER: 08/377,383
FILING DATE: 25-ANN-1995
APPLICATION NUMBER: 08/377,383
FILING DATE: 25-ANN-1994
APPLICATION NUMBER: 35046
TELECOMMUNICATION INCHARTION:
NAME: THOMAS G. WISSEMAN
REGISTRATION NUMBER: 35046
TELECOMMUNICATION INCHARTION:
TELEPAN: (202)861-3000
TELEFAN: (202)861-3000
TELEEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 224 base pairs
TTYPE: NUCLEIC acid
STRANDBORSS: 3ingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Other nucleic acid Synthetic DNA US-08-693-573-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-60-061-998-2/c

Sequence 2, Application US/60061998;
GENERAL INFORMATION:
APPLICANT: CORLEY, NEIL C.
APPLICANT: RUSSO, FRANK D.
APPLICANT: HANN, AMY L.
APPLICANT: HANN, AMY L.
APPLICANT: HANN, AMY L.
APPLICANT: HANN, AMY L.
APPLICANT: FINNY, GREGORY L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 GGGGCCTAACTAACTAATTTTGTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 GGGGCCCGGTACCCAGCTTTGTT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
```

요 ö

Search completed: May 30, 2000, 09:48:32 Job time: 60182 sec

gb_est26:*
gb_est27:*
gb_est28:*
gb_est29:*
em_est20:*
em_est21:*

gb_est30:*
gb_est31:*
gb_est32:*
em_est23:*
em_est24:*
em_est26:*

Seguence:

Run on:

Searched:

```
1001:::001:::002:::004:::004:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::000:::
                                                                                                                                                                                                                                        May 29, 2000, 21:13:16 ; Search time 2192.43 Seconds (without alignments) 277.310 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGCCAAAAATTGAAAAACTA......TTGTTTTTTGTGGGCCCGGCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9714632
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4857316 seqs, 2026611650 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                        US-08-935-377-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_est1:*
em_est2:*
em_est4:*
em_est5:*
em_est5:*
em_est5:*
em_est7:*
em_est8:*
em_est10:*
em_est10:*
em_est10:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_est18:*

9b_est1:*

9b_est3:*

9b_est4:*

9b_est5:*

9b_est6:*

9b_est6:*

9b_est6:*

9b_est6:*

9b_est1:*

9b_est11:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est17:*
gb_est18:*
gb_est19:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       em_est12:*
em_est13:*
em_est14:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            em_est16:*
em_est17:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est13:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est14:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      em_est15:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST:*
                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
```

Database :

gb_est45:*
gb_est46:*
gb_est47:*
gb_gss1:*
gb_gss2:*

gb_gss3:* gb_gss4:*

em_gss1:

9b_est33:**
9b_est34:**
9b_est34:**
9b_est34:**
9b_est36:**
9b_est38:**
em_est27:**
em_est29:**
em_est29:**
em_est29:**
em_est31:**
em_est31:**
em_est33:**
em_est33:**
em_est33:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

9b_gss12:*
9b_gss13:*
9b_gss14:*
9b_gss16:*

em_gss8:* gb_gss11:* gb_gss10:* em_gss9:*

gb_gss7:*
gb_gss8:*
gb_gss9:*

gb_gss6: em_gss5: em_gss6:

em_gss4: gb_gss5: em_gss3

em_gss10: em_gss11: em_gss12:

SUMMARIES

```
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Mark Adams
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
Department of Eukaryotic Genomics
Department of Eukaryotic Genomic Research
3712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 608)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J.,
Shizuya, H., Simon, M. and Venter, J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map
Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 GIGGAICCCCCGGGCTGCAGGAATICGAIAICAAGCITAICGAIACCGICGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ009167 608 bp DNA GSS , 27-JUN-1998 CIT-HFP-2281N13.TF CIT-HSP Homo sapiens genomic clone 2281N13, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAITGHHHHHHHHHHHHHHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        /sex="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 46.7%; Score 70; DB 96; Length 682; Best Local Similarity 93.6%; Pred. No. 1.4e-13; Matches 73; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Other_GSSs: CIT-HSP-2281N13.TR.1 CIT-HSP-2281N13.TF
CIT-HSP-2281N13.TR
                                                                                                                                                                                                                                                                                                                                                              1 others
                                                                                                                                                                                                                                                                                                                                                               ų
                                                                                                                                                                                                                                                                                                                                                              151
                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2301L23"
/clone_lib="CIT-HSP"
                                                                                                                                                                                  Location/Qualifiers
1. .682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 1. .608
                                                                                                                                                                                                                                                                                                                                                              187 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ009167
AQ009167.1 GI:3128599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 GGGGCCTAACTAACTAA 128
                                                                                                                                                                                                                                                                                                                                                            187 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 GGGGGCCGAGTACCCAA 1
                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
AQ009167/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                      AQ013255 CIT-HSP-2
AQ041198 CIT-HSP-2
T48593 ph6f4_19/1T
AA052885 T3551 Blo
B74162 CIT-HSP-202
                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ009153 CIT-HSP-2
AA752172 96BS0243
AQ074695 CIT-HSP-2
AQ008437 CIT-HSP-2
AQ014519 CIT-HSP-2
B72088 CIT978SK-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T26395 AB161A4F IN
B26269 F10B5TF IGF
A1239372 SWOVAFCAP
B53695 CIT-HSP-201
                                                                                                                                                                                                                                                                                        AQ012629 CIT-HSP-2
AQ012216 CIT-HSP-2
AQ012221 CIT-HSP-2
AQ009165 CIT-HFP-2
B6436 CIT-HFP-2
B70299 CIT-HSP-202
AQ016737 CIT-HSP-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 682)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Unpublished (1998)
Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                           B68775 CIT-HSP-205
B80296 CIT-HSP-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ012365 CIT-HSP-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Riftia pach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B65391 CIT-HSP-202
AQ024018 CPGR0359A
                                                                                                     2 CIT-HSP-201
147 AU037147
                                                                                                                                                                                                                                                      A0014512 CIT-HSP-2
B65534 CIT-HSP-202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2115 96BS0066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58116 SWAMCAC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ074693 682 bp DNA GSS 20-AUG-1998 CIT-HSP-2301L23.TF CIT-HSP Homo sapiens genomic clone 2301L23, genomic survey sequence.
                      Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D72088
                                                                                                     B54292
AU037147
                                                                                                                                                                                                                       AA052885
B74162
                                                                                                                                                                                                                                                                                                             2216
2221
9165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39372
                                                                                                                                                                                                                                                                                                                                                                                             10016737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40024018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ074693
AQ074693.1 GI:3436811
     Query
Match Length
                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.2
66
65.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65.4
62.8
62.2
62.2
60.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.8
57.8
57.4
57.2
56.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
AQ074693/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
     Result
                      Š
                                                        U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  υo
```

Gaps

ö

Indels

1;

```
Building
Unpublished (1997)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdddms@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: Mil Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 108)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Solden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .108
/organism="Homo sapiens"
/db_xref="GD8.7044003"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_12017M1"
/clone_11b="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                           B54292 108 bp DNA GSS 20-JUN-1998 CIT-HSP-2017M1.TR CIT-HSP Homo sapiens genomic clone 2017M1, genomic survey sequence.
                                                                                                                   Query Match 44.7%; Score 67; DB 84; I
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 67; Conservative 0; Mismatches 0;
Pred. No. 1e-12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 g
98.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B54292
B54292.1 GI:2608626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 c
Best Local Similarity 98.6
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                     111 GGGGGCCTA 119
                                                                                                                                                                                                                                       15 GGGGCCCA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 GGGGGCC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AU037147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                        RESULT
B54292
                                                                                                                                            В
                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٠ د....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Fibroblast"
/cell_type="Fibroblast"
/note="Vector: pBACLibrary A"
/note="Nector: pBACLibrary A"
/note: pBACLibrary A"
/not
                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B69688 528 bp DNA GSS 18-JUN-1998
CIT978SK-A-448E10.TVC CIT978SK Homo sapiens genomic clone A-448E10,
genomic survey sequence.
B69688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)

Contact: Mark Adams

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Email: madadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 528)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H., Simon, M. and Venter, J.C.
Use of a human BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism~"Homo sapiens"
/db_xxef="taxon:9506"
/db_xxef="taxon:9506"
/clone="2281N13"
/clone=11b="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/cell_type="Sperm"
/col_type="Sperm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                      Length 608
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                             ch 45.3%; Score 68; DB 96; 1
1 Similarity 100.0%; Pred. No. 6.6e-13;
68; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:5299607"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="A-448E10"
/clone_l1b="CIT978SK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 g
                                                                                                                                                                                                                                                               166 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B6968B.1 GI:2708912
GSS.
                                                                                                                                                                                                                                                                  164 c
                                                                                                                                                                                                                                 HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GGGGGCCT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111111
22 GGGGGCCT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118
                                                                                                                                                                                                                                                                  141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
B69688/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d
```

ö

0; Gaps

Length 528

84;

DB

Score 67.4;

44.98;

Query Match

Length 108; Indels

```
Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1to 114)

1 (bases 1to 114)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

1 Unpublished (1998)

1 Unpublished (1998)

1 Unpublished (1998)

2 Other_CSS: CIT HSP-2045D19.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
thtp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdddams@tigr.org
Clones are avallable from Research Genetics (info@resgen.com). BAC
and search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: MI3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B80294 144 bp DNA GSS 24-OCT-1998 CIT-HSP-2045D19.TR CIT-HSP Homo sapiens genomic clone 2045D19, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                         /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 44.7%; Score 67; DB 96; Length 14 Best Local Similarity 100.0%; Pred. No. 1.1e-12; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            35 t
                                                                                                                                                                                                 1. .141
/organism="Homo sapiens"
/db_xref="GDB:1103988"
/db_xref="taxon:9606"
/clone="2172N2"
/clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .144
/organism="Homo sapiens"
/db_xref="GDB:7054558"
/db_xref="taxon:9606"
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              41 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B80294.1 GI:2867317
                                                                                                                                                                                                                                                                                                                                                                                                                                 41 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                              24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 GGGGGCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                             Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
B80294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOCOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                   Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota, Dictyostellida, Dictyostellum.
Eukaryota, Dictyostellida, Dictyostellum.

( Dases 1 to 141)

Morlo, T., Urushihara, H., Salto, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitza, B.N., Pi, M., Sato, T., Takemoto, K., Yashikawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostellum developmental CDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 141)

Adams, M.D.; Rounaley, S.D.; Zhao, S.; Field, C.E.; Bass, S.; Linher, K.; Golden, K.; Berry, K.; Granger, D.; Suho, E.; Wible, C.; Shizuya, H.; Simon, M. and Venter, J.C.

Building (1998)
    AU037147 141 bp mRNA EST 29-WAR-1999
AU037147 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSB532, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lone_lib="Dictyostelium discoideum SS (H.Urushihara)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 GTGGATCCCCCGGGCTGCAGGAATTCGATGTGATTCAAGCTTATCGATACGTCGACGTCGAGCTTCATGATTCGATGATTCGAGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B95279 141 bp DNA GSS 26-JUN-1998 CIT-HSP-2172NZ.TF CIT-HSP Homo sapiens genomic clone 2172NZ, genomic survey sequence.
B95279 GI:2977616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan
Email: d402hu@askura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                       On Jan 19, 1998 this sequence version replaced gi:2153012.
Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Dictyostelium discoldeum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
44.7%; Score 67; DB 44; I
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Institute of Biological Sciences
University of Tsukuba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:44689"
/clone="SSB532"
                                                                                                                                                                                                                                                                                                                                development bNA Res. 5 (6), 335-340 (1998) 99156227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="slug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="AX4"
                                                                                            AU037147.1 GI:3983900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129 GGGGGCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
    LOCUS
DEFINITION
                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                            JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
COMMENT
                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
B95279/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
```

셤 ð 셤

ö

```
50 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 GGGGGCC 139
                                                                                          111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GGGGGCC 117
                                                                                                                GGGGGCC 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Si
Matches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                          41
                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                AQ041198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
T48593
                                                     셤
                                                                                        ò
                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Simon, M. and Venter, J.C.

Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,

Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

Other GSSs: CIT-HSP-2299C22.TR

Contect: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Email: mdadams@tigr.cor

Clones are availabe from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Sea primer: M13-21

Class: BAC ends.
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linher, K.,
                                                                                                                                                                                                                                                  51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                      70 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATATCGATACCGTCGACCTCGAGG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ013255 169 bp DNA GSS 06-JUN-1998 CIT-HSP-2299C22.TF CIT-HSP Homo sapiens genomic clone 2299C22.genomic survey sequence.
AQ013255 GI:3185820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                          /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                 ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                            Query Match 44.7%; Score 67; DB 84; Length 144; Best Local Similarity 100.0%; Pred. No. 1.1e-12; Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 44.7%; Score 67; DB 96; Length 16
Best Local Similarity 100.0%; Pred. No. 1.2e-12;
Matches 67; Conservative 0; Mismatches 0; Indels
                                                                                                           56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .169
/organism="Homo sapiens"
/db_xxef="GDB:7154018"
/db_xxef="taxon:9606"
/clone="2299C22"
/clone="2045D19"
/clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CIT-HSP"
                                                                                                           41 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                             43 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "IIIDUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                            130 GGGGGCC 136
                                                                                                                                                                                                                                                                                                                      111 GGGGGCC 117
                                                                                                           34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          uman.
                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
AQ013255/C
LOCUS
DEFINITION
                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                      ద
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidee; Homo.

1 (Dases 1 to 175)

2 Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berryy K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T48593 259 bp mRNA EST 02-FEB-1995 ph6f4_19/ITV Outward Alu-primed hncDNA library Homo sapiens cDNA clone ph6f4_19/ITV, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                   AQ041198 175 bp DNA GSS 14-JUL-1998 CIT-HSP-2335D21.TR CIT-HSP Homo sapiens genomic clone 2335D21, genomic survey sequence.
AQ041198 GI:3310469
                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.7%; Score 67; DB 96; I
llarity 100.0%; Pred. No. 1.2e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .175
/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="2335021"
/clone="Lb="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 9
```

```
Fax: 254 2 631 499
Email: a.osanya@cgnet.com
Seq primer: M13 primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B74162
B74162.1 GI:2769849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 GGGGGCC 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
B74162/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .259
/organism="Homo sapiens"
/do_aref="texter" texter" texter="texter" texter="texter" texter="texter" texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="texter="tex
                                                                                                                               Eukaryofa; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 259)

1 (bases 1 to 259)

Vinogradova, T.V., Lebedev, Y.B., Kopantzev, E.P., Wagner, L.L., Volik, S.V., Ermolaeva, O.D., Lavrentyeva, I., Monastyrskaya, G.S. and Sverdlov, E.D.

Outward Alu-primed hncDNA library

Unpublished (1995)

Contact: Sverdlov ED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO52885 275 bp mRNA EST 13-SEP-1996
13551 Bloodstream form of serodeme ILTatl.1 Trypanosoma brucei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osanya, A., Murphy, N.B. and Pelle, R.
Trypanosoma brucei brucei cDNAs
Unpublished (1996)
ON Nov 29, 1993 this sequence version replaced gi:637578.
Contact: Osanya A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trypanosoma brucei brucei.
Trypanosoma brucei brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Structure and Function of Human Genes
Shemyakin Institute of Bioorganic Chemistry
16/10 Miklukho-Maklaya, Moscow, 117871, Russia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

44.7%; Score 67; DB 20; L
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        International Livestock Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 70953306529
Fax: 70953306538
Email: sverd@humgen.siobc.msk.su.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brucei cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Box 30709, Nairobi, Kenya
Tel: 254 2 630 743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA052885.1 GI:1543898
                              GI:642793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma.
1 (bases 1 to 275)
                                                                                                                   Homo sapiens
T48593
T48593.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 GGGGGCC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
ACCESSION
                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
/strain="Colone A4"
/db.xref="taxon:5702"
/clone_11b="Bloodstream form of serodeme ILTatl.1"
/clone_11b="Bloodstream form of serodeme ILTatl.1"
/clone_11b="Bloodstream form of serodeme ILTatl.1"
/note="colone A4"
/note="colone A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mdadam@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq Primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 386)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 GIGGAICCCCCGGGCIGCAGGAAIICGAIAICAAGCIIAAICGAIACCGICGACCICGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B74162 386 bp DNA GSS 24-0CT-1998 CIT-HSP-2028NI.TF CIT-HSP Homo sapiens genomic clone 2028NI, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 44.7%; Score 67; DB 27; Length 275; 1. Similarity 100.0%; Pred. No. 1.3e-12; 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Other GSSs: CIT-HSP-2028NI.TR
Ocheart: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 0208
/organism="Trypanosoma brucei"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .386
/organism="Homo sapiens"
/db_xref="GDB:7048251"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence tags.
```

BASE COUNT ORIGIN

Best Loca Matches

ð ద

```
124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          547 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B65534.1 GI:2639512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "IIIDUTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                             111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQ012629
                                                                                                                                                                                                                        39 GGGGGCC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 GGGGGCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1:
AQ012629
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SION
                                                                                                                                                                                                                                                                                                                                                     B65534/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                               8
                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 462)

4 (Dases I to 462)

6 Golden, K., Rounaley, S. D., Zhao, S., Field, C. E., Bass, S., Linher, K., Simon, M. and Venter, J. C.

5 Simon, M. and Venter, J. C.

10 Ge of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
and Search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mill 21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ014512 462 bp DNA GSS 06-JUN-1998 CIT-HSP-2300D21.TF CIT-HSP Homo sapiens genomic clone 2300D21, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
/db_xref="taxon:9606"
/clone="2028NI"
/clone="lb="CIT-HSP"
/sex="Male="
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Sperm"
//note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                               ch 44.7%; Score 67; DB 84; Length 386; I Similarity 100.0%; Pred. No. 1.3e-12; 67; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
The Institute for Genomic R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
44.7%; Score 67; DB 96; I
Rest Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 67; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ų
                                                                                                                                                                                                                            ų
                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:7154425"
/db_xref="taxon:9606"
/clone="2300D21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                        109 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ014512
AQ014512.1 GI:3184839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Male"
                                                                                                                                                                                                                            98
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "IIIputH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                               Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 GGGGGCC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 GGGGGCC 16
                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Local
```

RESULT 13 AQ014512/c

ŏ g LOCUS

ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL COMMENT

TITLE

```
The institute for Genomic Research Genetics (info@resgen.com). BAC Genomes are are an all and answer of the search in the search periods are are all and answer.

The institute for Genomic Research grant in the institute for Genomic Research grant of Eukaryotic Genomics.

The institute for Genomic Research grant grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21
Class: BAC ends.
51 GTGGATCCCCCGGGCTGCAGGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B65534 519 bp DNA GSS 21-JUN-1998 CIT-HSP-2022D24.TF CIT-HSP Homo sapiens genomic clone 2022D24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:7045730"
/db_xref="CDB:0045730"
/clone="2022024"
/clone_lib="CIT-HSP"
/cell_type="Sperm"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 67; Conservative 0; Mismatches 0;
```

ö

BASE COUNT ORIGIN

FEATURES

```
Eutheria: Primates; Catarrhini; Hominidae; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

E 1 (Dases 1 to 547)

S ddams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

L Unpublished (1998)

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mdadams@tigr.org
Clones are availabe from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
CIT-HSP-2299F1.TR CIT, HSP Homo sapiens genomic clone 2299F1, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="2299f1"
/clone_lib="cir-HSp"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 g
                                            AQ012629
AQ012629.1 GI:3185194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                    ORGANISM
                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                     JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES .
                                                                                                                                                                                                                                                                                           TITLE
```

ŏ d

ö

0; Gaps

Length 547; Indels

Query Match 44.7%; Score 67; DB 96; L Best Local Similarity 100.0%; Pred. No. 1.4e-12; Matches 67; Conservative 0; Mismatches 0;

111 GGGGGCC 117

ö

135 GGGGGC 141 g

Search completed: May 29, 2000, 21:13:17 Job time: 36516 sec